





Sequence 2733 BP; 823 A; 633 C; 624 G; 653 T; 0 other,

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alignment_block:
US-08-917-710-2 x AAA09048
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Align seg 1/1 to: AAA09048 from: 1 to: 2733

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1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyLysLeuGlu 17
2 1 :::::
3 1 AAGGCTCTCTGTGGTGGTGTAGTGAATCTCTACTTTTATGGAACTCGCA 50
4
5 17 nSerAspAlaSerGluArGcysAspAspTrpGlyLeuAspTrpMetArg 34
6
7 51 AAGTAGATGCGCTCAGAACGCGTGATGACTGGGAGACTAGACACCATGAGGC 100
8
9 34 InILGlyValIheGluAspGluProAlaArgLysCysProLeuPhe 50
10 101 AAATCCAACTGTTTAAAGATGAGCCAGCTCGCATCAAGTGCACACTCTTT 150
11
12 51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeuTh 67
13
14 151 GAACACTTCTTGAANTTCACACTACAGACAGCCACTTACGCTGGCTTTAC 200
15
16 67 rLeuLeuTrpTrpTrpTrpLysGlnAspArgAspLeuGluGluProIleA 84
17 201 TCTGATCTGATGATTTGGACAGACGAGACCGGGGACCTTGAGAGCCAAATT 250
18
19 84 snPheArLeuProGluAsnArgLysSerLysGluLysAspValLeuTrp 100
20 251 ACTTCGCCCTCCCCGAGAACCCGACTTAGTAAAGAGAAAGATGTGCTGTGG 300
21
22 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpTrpCysMetLeuArg 117
23 301 TTTCGGGCCACTCTCTCTCAATACACTGCGCACTATACCTGGATGTTTAA 350
24 117 GasnThrThrTrpCysSerLysValAlaPheProLeuGluValValGlnL 134
25 351 GAACACTCAATATTCACACCAAGTGGCATTTTCCCTGGGAAGTTGTTCAAA 400
26 134 yAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTrp 150
27 401 AAGCAGCTGTTTCATATTCGCCCAAGAACTCCAGTGCAATAACTGAT 450
28 151 IleGluTrpGlyLysLeuArgIleThrCysProAsnValAspGlyTrpPh 167
29 451 ATAGATATATGCATTCAGAGATCACTTGTCGCAAAATGTAGATGAGATATT 500

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167	eproSerSerValIysProThrIleThrTPtryrMeGlyysrIylsI	184
501	TCCTTCACGTGTAACCCGACTATCACTGGTAATAGGGCTTATAAA	550
184	IecIAsnPheAsnAsnValIleProGluGlyMeTAsnLeuSerPheLeu	200
551	TACAGAAATTTTAAATATGTATATACCCGAGATGAACTTAGTTCCCTC	600
201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValIThrTyrPr	217
601	ATTTGCTTATTTTCAATAATATGAAAAATTACACATGTGTGTGTACATATCC	650
217	ocIuAsnGlyArgThrPheHisLeuThrArgThrLeuThrValIlyValI	234
651	ACAAAAATGACGACGTACCTTTTCATCTCACAGGACTCTCACTGTAAAGTAG	700
234	aIGlySerProIysAsnAlaValProProValIleHisSerProAsnAsp	250
701	TAGGCTCTCCAAAAAATGACAGTCCCTCCCTGTGATCCATTCACCAATATGAT	750
251	HisValValTyrGluIuysGluProGlyGluGluLeuLeuIleProCysTh	267
751	CATGTGGCTATGACAAAGAACAGAGAGAGAGACTACTCAATCCCTGTAC	800
267	rValTyrPheSerPheLeuMetAspSerTrgAsnGluValTyrTPtrPhrI	284
801	GGTCATATTTTACTTTTCTGATGATCTCGCATATGAGGTTGGTGGACCA	850
284	IeAsGlyIlyIysProAspAspIleThrIleAspValThrIleAsnGlu	300
851	TTGATGAAAAAAACCTCATGACATCATCATATGTATGATCATCACTTAACGAA	900
301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSe	317
901	AGTATATGATCATATGATAGAACACAGATGAAACAGAACTCAGATTTTGAG	950
317	rIleIysIysValIThrSerGluAspLeuIysArgSerTyrValCysHisA	334
951	CATCAAGAAAGTTACTCTGAGGATCTCAAGCGCACCTATGTCTGCATG	1000
334	IaArgSerAlaIysGlyIuValAlaIysAlaIalysAlaIysValIysGlnIys	350
1001	CTAGAGAGTGCACAAAGGCGAAGTTGCCCAAGACCCCAAGGTGAAGCAGAAA	1050
seq_name: /SDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AAAT320227		
seq_documentation_block:		
ID	AAAT32027 standard; cDNA; 1077 BP.	
AC	AAAT32027;	
XX		
DT	14-OCT-1996 (first entry)	
XX		
DE	Soluble interleukin-1 receptor accessory protein cDNA.	
XX		
KM	Interleukin-1 receptor accessory protein; IL-1 antagonist;	
KW	inflammation; therapy; antiinflammatory; ss.	
XX		
OS	Synthetic.	
XX		
EH	Key	Location/Qualifiers
FT	sig_peptide	1..60
FT	mat_peptide	/*tag= a
FT		61..1077
FT		/*tag= b
XX		
PN	W09623067-A1.	
PD	01-AUG-1996.	
XX		
PF	17-JAN-1996;	96WO-EP00181.
XX		



	134	ysaspsrCysPheasnSerPrometLysleuProValHisIstysLeuyr	150
	401	AAGGACCTTTTCATTCATCCCATTAACCTCCAGTGCATAAAGCTAT	450
	151	IleGlutryGIylIleGlnArgIlethrCysProasnValaspolytyrPh	167
	451	ATGAAGAATATGGCAATTGAGAGATCACTTGCCAAATGTGATGATATT	500
	167	eProserSerValLysProthrIlethrTrptrymetgLyCystYrlysi	184
	501	TCCCTCCAGTGTAAACCAGACTATCACTTGATATAGGGCTGTATTAAA	550
	184	legInasnpheasnAsnValIleProgluglYmetAsnLeuSerPheleu	200
	551	TACAGATTTTATATGTAATACCGAAGATATGACTTGAGTTCTCTC	600
	201	IleAlaleuileSerAsnsglysnTyrrhCysvalValThrTYPr	217
	601	ATTGCCCTTATTTCMAATATGGAATTCACATGTGTTGTATCATATCC	650
	217	oGUAsnglyArgThrPheHisIstenthrArgthrleuthrVallysValy	234
	651	AGAAATGGAGCGACTTTCATCTCACCGAGACTGTGACTGTAAAGTAG	700
	234	aGlyserProlysasnaIalavalProProValIleHisSerProasnsp	250
	701	TAGGCTCTCAAAAAATGACGTGCCCCCCHGTGATCATTCACCTAATGAT	750
	251	HIsValValThyGluIuysGluProgluglUleuIeuIleProCysTh	267
	751	CATGGTGCTATAGAAAGAACCGAGAGGAGCTATCATTCATTCCTGTAC	800
	267	rValTyrrheserPheLeuMetAspSerArqasnIuValTrpTryphri	284
	801	GGCTATTATTAGTTTCTGATGGATTTCGCAATGAGTTGGTGGANCA	850
	284	leaspolyLysIysProaspapIlethrIleaspValThrIleasnGlu	300
	851	ITGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA	900
	301	SerIleSerHisSerArgThrGluuspIuThrArgTrghIleleuse	317
	901	AGATATAGTCATAGTAGAACAACAAGATGAACAAAGAACTCGATTTTGAG	950
	317	rIleLysIysValIthrSergIuasPleullysArgsetTyrrValcYshIsa	334
	951	CATCAGAAAGTTACCTCTGAGGACTCTCAACGCGAGTATCTGTGTCATG	1000
	334	laarSerAlaysgIyGluIuValAlalytsAlalyvalIysValyGlyLys	350
	1001	CTAGAGTGCCCAAGCGCAAGTGGCCAAGCAAGCCAAAGTGACGCAAGAAA	1050
seq_name:	/SIDS1/gcgcdata/geneseq/geneseqn-emb1/NN196.DAT:AAT32028		
seq_documentation_block:	ID AAT32028 standard; CDNA: 1713 BP.		
AC	AAT32028;		
XX			
XX	14-OCT-1996 (first entry)		
DT			
XX			
DE	Mouse interleukin-1 receptor accessory protein cDNA.		
XX			
KW	Interleukin-1 receptor accessory protein; IL-1 antagonist;		
KM	Inflammation; therapy; antiinflammatory; ss.		
XX			
OS	Mus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	sig-peptide	1..60	
FT		/tag- a	
FT	mat-peptide	61..1710	
FT		/tag- b	

XX W09623067-A1.  
 XX 01-AUG-1996.  
 XX 17-JAN-1996; 96WO-EP00181.  
 XX 23-JAN-1995; 95US-0376268.  
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX Chlazonite RA, Ju GM;  
 XX WPI: 1996-362691/36.  
 XX P-PSDB; AAM01913.  
 XX Isolated interleukin-1 receptor accessory protein - used to develop  
 XX prods. to treat or prevent inflammatory or immunological activities  
 XX of interleukin-1  
 XX  
 XX Example 7; Page 76-77; 115pp; English.  
 XX A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor  
 XX accessory protein (IL-1R ACP), a protein that inhibits the  
 XX ability of IL-1 to bind to, or otherwise activate, the IL-1R,  
 XX esp. the type 1 IL-1R. It was obtd. by screening cell-surface  
 XX proteins in COS-7 cells transfected by 3T3-IL cDNA using  
 XX anti-murine IL-1R ACP monoclonal antibody 4C5, and isolation of  
 XX cDNA clones from positive lines. The murine cDNA was used to  
 XX obtain a partial genomic clone of the human homologue. A probe  
 XX derived from this genomic clone was then used to isolate the  
 XX full-length cDNA (AAT32026) for human IL-1R ACP (AAM01911).  
 XX  
 XX Sequence 1713 BP; 473 A; 386 C; 428 G; 426 T; 0 other;

alignment\_scores:  
 Quality: 1660.00 Length: 350  
 Ratio: 4.955 Gaps: 0  
 Percent Similarity: 95.714 Percent Identity: 84.857

alignment\_block:  
 US-08-917-710-2 x AAT32028 ..

Align seg 1/1 to: AAT32028 from: 1 to: 1713

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 1 ATGGGACTTCTGTGTATTTGATGAGTCTGTCTCTATGAGATCCGCA 50  
 17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34  
 51 GAGTCATGCTTCGAGCGCTGTGTATGACTGGGACTGATATACCATGGAC 100  
 34 InIleGlnValPheGluAspGluProAlaArgIleGlyCysProLeuPhe 50  
 101 AATCCAAAGTGTGGAAGATGAGCGGCTGCAATCAAGTGCCTCTTTT 150  
 51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerIleGlyLeuTh 67  
 151 GAACACTTCTCGAAGTACACTACAGCATGCCCCATTCTCTGCTTAC 200  
 67 rLeuIleTrpTrpThrLysGlnAspArgAspLeuGluGluProIleA 84  
 201 CCGATCTGCTGACTGACCAAGCAAGACCGGACCTGGAGAGCCCATTA 250  
 84 snPheArgLeuProGluAsnArgIleSerLysGlyLysAspValLeuTrp 100  
 251 ACTTCGCCCTCCAGAGATCGCATCAGTAAGAGAAAGATGCTCTGG 300  
 101 PheArgProThrLeuAsnAspThrGlyAsnTrpTrpCysMetLeuAr 117  
 301 TTCGGGCCCTCTCTCAATGACAGGGCAATTACACTCTCATGTTGAG 350

117 gAsnThrThyrcysSerLysValAlaPheProLeuGluValValGlnL 134  
 351 GACACAACTTACTGACCAAGCAAGTTCATTTCCCTGGAAGTGTGAGA 400  
 134 ysAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTr 150  
 401 AGGACAGCTGTTTCAATTCCTGCATGAGATTCCTCCAGTGCACAGATGTAT 450  
 151 rLeuGlyTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTrp 167  
 451 ATTGAAATGCTTCATATGATGATGATGATGATGATGATGATGATGAT 500  
 167 eProSerSerValLysProThrIleThrTrpMetGlyCysTrpLysI 184  
 501 TCCTTCACAGTGTCAACATGCGTGTGATTAAGGTTGATGATAA 550  
 184 rLeuAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
 551 TAGTGACTTTCATATGATGATGATGATGATGATGATGATGATGAT 600  
 201 rLeuAlaLeuIleSerAsnAsnGlyAsnTrpTrpCysValValTrpTrp 217  
 601 ATCCCTTGTTGTTCAATTAACGGAATTAACATGATGATGATGATGAT 650  
 217 GlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234  
 651 TGAAAGAGGAGCTGCTTCACTCACCAGCAGTGTGCTGCTGCTGCTG 700  
 234 aGlySerProLysAsnAlaValProProValIleHisSerProAsnAsp 250  
 701 TGGGCTCACAAAGATGATGATGATGATGATGATGATGATGATGATG 750  
 251 HisValValTrpGlyLysGluProGlyGluGluLeuLeuIleProCysTh 267  
 751 CGTGTGCTGATGAGAAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAG 800  
 267 rValTrpPheSerPheLeuMetAspSerArgAsnGluValTrpTrpTr 284  
 801 AGCTATATTCAAGTTCATATGATGATGATGATGATGATGATGATGAT 850  
 284 rAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
 851 TTGATGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 900  
 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSe 317  
 901 AGTGTAGTATTATTCTTCAACGAGATGAAACAGAGCTCAGATTGTGAG 950  
 317 rIleLysLysValThrSerGluAspLeuLysArgSerTrpValCysHis 334  
 951 CATCAAGAAAGTCAACCCGAGGATCTCAGGCGCAACATGCTGTCTATG 1000  
 334 rArgSerAlaLysGlyGluValAlaLysAlaLysValLysGlnLys 350  
 1001 CTCGAATATCCAAAGGAGAGAGTGAAGAGCTGCCAAGGTGAACAGAA 1050

seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AA124540

seq\_documentation\_block:  
 ID AA124540 standard; DNA; 287 BP.  
 XX AA124540;  
 AC 12-OCT-2001 (first entry)  
 DE Probe #14473 for gene expression analysis in human cervical cell sample.  
 XX Probe: human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer; ss.  
 XX Homo sapiens.  
 XX

PN WO200157278-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488901/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 XX analyzing gene expression in human cervical epithelial cells -  
 XX  
 PS Claim 25; SEQ ID No 14473; 487pp; English.  
 XX  
 CC The present invention relates to human single exon nucleic acid probes  
 CC (SENPs). The present sequence is one such probe. The SENPs are derived  
 CC from human HeLa cells. The SENPs can be used to produce a single exon  
 CC microarray, which can be used for measuring human gene expression in a  
 CC sample derived from human cervical epithelial cells. By measuring gene  
 CC expression, the probes are therefore useful in grading and/or staging  
 CC of diseases of the cervix, notably cervical cancer.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SO Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other.  
  
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 Ratio: 5.558 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.947  
  
 alignment\_block:  
 US-08-917-710-2 x AAI24540 ..  
  
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 23 ArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheG1 39  
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 3 CGCTGCCGATGACTGGGACTAGACCCATGAGGCAAAATCCAAAGTGTGGA 52  
  
 39 uAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysP 56  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 53 AGATGAGCCAGCTGCGATCAAGTGCCTTTGAAACACTTCTTGAAT 102  
  
 56 heAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrT 72  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 103 TCACTACAGCAGCAGCCCATTCAGCTGCTTACTCGATCGATGCTATTGG 152  
  
 73 ThrLysGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProG1 89  
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 153 ACTAGGCGAGACCGGACCTTGAGAGAGCCATTAACCTCCGCCCTCCCGA 202  
  
 89 uAsnArgIleSerLysGluLysAspValLeuTyrPheArgProThrLeu 106  
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 203 GAACCGCATTAAGTAAAGAAAGATGCTGTGTTCCGCCCTCCCTCTCC 252  
  
 106 euAsnAspThrGlyAsnTyrThrCysMetLeuArg 117  
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seq\_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAI49786  
 seq\_documentation\_block:  
 ID AAI49786 standard; DNA; 287 BP.  
 XX  
 AC AAI49786;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Probe #18472 used to measure gene expression in human placenta sample.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00663.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-48897/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 XX analyzing gene expression in human placenta -  
 XX  
 PS Claim 25; SEQ ID No 18472; 654pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes (SENPs).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders.  
 XX  
 SO Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other.  
  
 alignment\_scores:  
 Quality: 528.00 Length: 95  
 Ratio: 5.558 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 98.947  
  
 alignment\_block:  
 US-08-917-710-2 x AAI49786 ..  
  
 Align seg 1/1 to: AAI49786 from: 1 to: 287  
  
 23 ArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheG1 39  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 3 CGCTGCCGATGACTGGGACTAGACCCATGAGGCAAAATCCAAAGTGTGGA 52  
  
 39 uAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysP 56  
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 53 AGATGAGCCAGCTGCGATCAAGTGCCTTTGAAACACTTCTTGAAT 102  
  
 56 heAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrT 72  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 103 TCACTACAGCAGCAGCCCATTCAGCTGCTTACTCGATGCTATTGG 152  
  
 73 ThrLysGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProG1 89

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153 ACTAGGACGACCGGAGCCTTGAGAGCAATTAACCTCCGCCCGCA 202
89 uasnaarglleserlysglulysaspvalleutrphearprothleul. 106
|||||
203 GAACCGCATTTAGTAAGAGAAAGATGTGCTGCGGCCACACTCTCC 252
106 euasnaasphtrglyasntrythrlyscysmetleuarg 117
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253 TCATGTACACTGGCACTATACCTGCATGTAAAG 287
seq_name: /SIDSI/gcdata/geneseq/geneseqn-emb1/NA1999.DAT.AAX58245

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seq\_documentation\_block:

ID AAX58245 standard; CDNA: 2061 BP.

AAK58245;

22-JUL-1999 (first entry)

Human IL-1RD8 coding sequence.

IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNAX; therapy;

IL-1 receptor-like protein; abnormal expression; immunological disorder;

inflammatory disorder; morphological disorder; ss.

Homo sapiens.

WO919480-A2.

22-APR-1999.

14-OCT-1998; 98WO-US20939.

10-AUG-1998; 98US-0095987.

15-OCT-1997; 97US-0951829.

17-NOV-1997; 97US-0971635.

12-MAR-1998; 98US-0078008.

18-MAR-1998; 98US-0040714.

15-APR-1998; 98US-0081883.

(SCHE) SCHERING CORP.

Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;

WPI: 1999-326545/27.

P-PSDB; AAY14128.

Interleukin-1 receptor-like polypeptides RD8, 9 and 10

Claim 28; Page 93-96; 150pp; English.

This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide,

designated IL-1 receptor DNAX designation 8 (IL-1RD8), of the

invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, of the

and mutants, also related antibodies, other binding agents and

(ant)agonists are used to treat conditions associated with abnormal

expression of the polypeptide or abnormal expression of, or response to,

their ligands, e.g. immunological, inflammatory or morphological

disorders. They may also be used to screen for binding agents (potential

drugs), diagnostic reagents (to detect the proteins or their ligands) and

to isolate related sequences. Antibodies may also be used to raise

anti-idiotypic antibodies, as carriers for toxins, radionuclides or other

therapeutic agents, and for affinity purification.

Sequence 2061 BP; 656 A; 421 C; 459 G; 525 T; 0 other;

alignment\_scores:

Quality: 438.50 Length: 369

Ratio: 1.975 Gaps: 15

Percent Similarity: 60.163 Percent Identity: 31.978

alignment\_block:

US-08-917-710-2 x AAX58245 ..

Align seg 1/1 to: AAX58245 from: 1 to: 2061

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16 uGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMet 33
|||||
69 AAAGAGAAATTCCTGTGATGAGCTCATTGACTGGTGTGAT...CTCA 115
33 rGlnIleGlnValPheGluAspGluProAlaArgIleLeuCysProLeu 49
|||||
116 AGACATATATGCTTTGGCAGCTGACGACGACGACGACGACGACGACCTT 165
50 PheGluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLe 66
|||||
166 TTCTACAGTATATTCGTACCACTATAGCACGCGCCAGACGACGACGCT 215
66 uThrLeuLeuTrpTrpTrpThrLysGlnAspArgAspLeuGluProI 83
|||||
216 CAGCTTATGTGTATC.....AAAACAAGGTGATTGGAAAGCCCA 259
83 LeAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeu 99
|||||
260 TCATCTTT.....TCAGAGCTCAGGATGACGACGACGACGACGACGAT 303
100 TrpPheArgProThrLeuLeuAsnAspThrLysAsnTrpCysMetLe 116
|||||
304 TGGTTTCACCTGCTGAGGACGACGACGACGACGACGACGACGACGCTTT 353
116 uArgAsnThrTrpTrpCysSerLysValAlaPheProLeuGluValG 133
|||||
354 AAGCAATCAATCATATTCATGAAAGGTGATGCTGCTGCTGCTGCTGCTG 403
133 LeuLysAspSer.....CysPheAsnSerProMetLysLeuProValHis 147
|||||
404 AGAATGAATCAAGCCTGTGCTACAAACAGCAGATCCG..... 441
148 LysLeuTrpIleGluTrpGly.....IleGlnArgIleThrCys 160
|||||
442 .....TATTGAAATAATCTGAATCACTATAAAGAGAGATCCCTG 485
160 sProAsnValAspGlyTrpPheProSerSerValLysProThrIleTrp 177
|||||
486 TCCAGACATGATGATGACTTAAAGAGTCCGATCAGGACGCTGATGTCGT 535
177 rPyrMetGlyCysTrpLysIleGlnAsnPheAsnAspValIleProGlu 193
|||||
536 GGTATTAAGAAATGCAAGCCAAAATGTGAGAGCAATATATATACAGAA 585
194 GlyMetAsnLysSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTrp 210
|||||
586 GGAATAGCTCTTCTGATCCAGAGATTCAGAGAAAGATGAGGAAATTA 635
210 rThrCysValValThrTrpProGluAsnGlyArgThrPheHisLeuTrp 227
|||||
636 CACATGTGAACCTTAATAT.....GAAAGAAACCTT.....GTAAAGC 673
227 rGthrLeuThrValLysValIleGlySerProLysAsnAlaValPro... 242
|||||
674 GAACAACTGAATTAAGAGTTACAGCTTCTACACAGACAGAGCTCCCAAG 723
243 ProValIleHisSerProAsnAspHisValValTrpGluLysGluProG 259
|||||
724 CCAATGTCCTCCCAATGAGATCAGCAAGCTGTTATAGATGTCACACTGG 773
259 yGluGluLeuLeuIleProCysThrValTrpPheSerPheLeuMetAsp 276
|||||
774 TAAGCCTTGAAACATCCCTCGCAAGCAATTCCTGGATTCAGTGAGAGT 823

```



disorders. They may also be used to screen for binding agents (potential drugs) diagnostic reagents (to detect the presence of a disease) and

203 nyl m cys val val m yl p r o g i u a s n g l y a l g i n l p l e n i s l e u t 22

618 TTACACATGTGAAGCTTAATAT.....GAAGGAAACTT.....GTAA 651

```

226 hrargThrleuThrValIysValIleGlySerProLysAsnAlaValPro 242
      ||||| .....
656 GAGCAACACATGATGTAAGTTACACTTACACAGAACAGCCCTCC 705
      ||||| .....
243 ...ProValIleHisSerProAsnAspHisValValTyrGluGluP 258
      ||||| .....
706 AAGCATTGTTCCCATGAGAAATCACCACCAAGTTATGATGTCGACGT 755
      ||||| .....
258 oGluGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMet 275
      ||||| .....
756 GGGTAAGCCTTGACATCCCTCCAAAGCATTTTCGATTCAGTGCAG 805
      ||||| .....
275 sPSeArGAsnGluValTyrTrpThrIleAspGlyLysProAsp 291
      ||||| .....
806 AGTCTGGCCCAATGATCTACTG...ATGAAGAGAGAAAG... 843
      ||||| .....
292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThr 308
      ||||| .....
844 .....TTATTGAGAACTGGCAGGTCACTTGA...GA 875
      ||||| .....
308 uAspGluThrArg.....Thrg 314
      ||||| .....
876 AGGGAATATAGGCTTCTCAAGACATCTTGAGAAAGAAAGTTGAT 925
      ||||| .....
314 InIleuSerIleLysLysValThrSerGluAspLeuLysArgSerTyr 330
      ||||| .....
926 TGGCAGCTCATCTTGACTGACGTTGAGAGCTGACCTG...GCCAATTAT 972
      ||||| .....
331 ValCysHisAlaArgSerAlaIleGlyGluValAlaIleLysVal 347
      ||||| .....
973 ACCTGCCATGTTGAAACCGAATGAGAGGAACATGCCAGTGTTCCT 1022
      ||||| .....
1023 GCGTAAAG 1032

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seq\_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAx84308

seq\_documentation\_block:

ID AAX84308 standard; DNA: 1979 BP.

AC AAX84308;

DT 08-SEP-1999 (first entry)

XX Human TIGIR coding sequence.

DE TIGIR: human; chromosome X; FG syndrome; premature ovarian failure-1;

KW leiomyomatosis; epilepsy; Bazex syndrome; detection; defective gene;

KW cell-signal transduction; gene therapy; inhibitor; immune regulation;

KW cell proliferation; inflammation; ss.

OS Homo sapiens.

PN W09932629-A1.

PD 01-JUL-1999.

PF 23-DEC-1998; 98WO-US27625.

PR 23-DEC-1997; 97US-0068634.

XX (IMMV ) IMMUNEX CORP.

PI Sims JE;

DR WPI, 1999-418928/35.

DR P-PSDB; AAY22164.

XX New interleukin-1 receptor analog TIGIR nucleic acid and proteins

PT used to, e.g. treat autoimmune disease

XX Claim 1; Page 8-9; 79pp; English.

```

XX This sequence encodes the human TIGIR protein of the invention. The
CC TIGIR DNA sequences can be used: (a) as probes or primers for
CC identifying nucleic acid that encodes proteins with TIGIR activity;
CC (b) to identify human chromosome X, to map genes on this chromosome
CC and to identify disease-related genes (particularly in the region
CC Xq21.3-22 where genes are present associated with e.g. FG syndrome,
CC premature ovarian failure-1, leiomyomatosis, epilepsy, Bazex syndrome
CC etc.) including detection of defective genes; (c) to study cell-signal
CC transduction and the TIGIR system, and (d) in gene therapy. Sense and
CC antisense oligonucleotides derived from the TIGIR coding sequence can be
CC used to inhibit expression of the TIGIR gene. The TIGIR protein, or its
CC soluble fragments, are used: (1) to study cellular processes (immune
CC regulation, proliferation, death, migration, interaction with other cells
CC and inflammation); (1i) to identify and purify proteins that associate
CC with TIGIR ligands and receptors, and to measure their biological
CC activity; (1ii) in screening for, and rational design of, potential
CC inhibitors of activity; (1v) therapeutically against diseases mediated by
CC TIGIR polypeptide counter-structures; (v) as molecular weight markers in
CC electrophoresis; (vi) for determining isoelectric points of unknown
CC proteins; (vii) as controls for determining the extent of protein
CC fragmentation (e.g. to aid characterisation of protein structures by mass
CC spectrometry); (viii) for generation of antibodies (Ab); and (ix) to
CC deliver diagnostic or therapeutic agents to cells that express TIGIR
CC binding molecules. Ab are used for affinity purification of TIGIR;
CC therapeutically to inhibit binding of TIGIR to its counter structures,
CC and (if agonistic) to promote cell signalling.
XX
SQ Sequence 1979 BP; 636 A; 405 C; 439 G; 499 T; 0 other;

```

alignment\_scores: Quality: 431.00 Length: 345  
Ratio: 2.072 Gaps: 14  
Percent Similarity: 60.290 Percent Identity: 32.754

alignment\_block:

US-08-917-710-2 x AAX84308 ..

Align seg 1/1 to: AAX84308 from: 1 to: 1979

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24 CysAspAspTrpGlyLeuAspThrMetArgGlnIleGluValPheGluAs 40
||| ||||| .....
9 TGCATTGACTGTGCTAGTGAT...CTCAAGACATACATAGCTTGGCAGG 55
||| ||||| .....
40 pGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPhe 57
||| ||||| .....
56 TGACACAGCCGAGTGAATGTCCTTTTACAGTATATTCGTACCA 105
||| ||||| .....
57 sNtySerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThr 73
||| ||||| .....
106 ACTATAGCAGCGCCGACGACTGGCTCAGCTTATGTGTAC..... 149
||| ||||| .....
74 LysGluAspArgAspLeuGluIleProIleAsnPheArgLeuProGluAs 90
||| ||||| .....
150 AAAACCAAGGTGATTTGGAAGACCCATCATCTT.....TCAGAGCT 193
||| ||||| .....
90 nArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeu 107
||| ||||| .....
194 CAGGATGACCAAGAGAGATTCATATGTTTCACGACGCTGAGGAC 243
||| ||||| .....
107 sNAspThrGlyAsnTyrThrCysMetLeuArgAsnThrTyrCysSer 123
||| ||||| .....
244 AAGACAGTGAATTCACCTGTGTTTAAAGAACTCAACATATGTCATG 293
||| ||||| .....
124 LysValAlaPheProLeuGluValAlaGlnLysAspSer.....CysPh 138
||| ||||| .....
294 AAGGTGTCATATGCTTGTGAGAGATGATGAGGCTGTGCTA 343
||| ||||| .....
138 eAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
||| ||||| .....
344 CAACACGACAGATCCG.....TATTAGAAATATCG 375
||| ||||| .....

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155 .....IleGlnArgIleThrCysProAsnValAspGlyTyrPhe 167
376 AAGTCACATAAAGAAAGAGATCTCTGCTCCAGACATGATCACTTAA 425
168 ProSerSerValLysProThrIleThrIleThrIleThrIleThrIle 184
426 AAGTCGATCAGAGAGCTGATGTTGTGTATGAAGATGCAAGCCAA 475
184 eGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 201
476 AATGTGGAGAACCATATATATACAAAGAAATCTCTTGATCCAG 525
201 LeuIleLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
526 AAGTTCAGAGAAAGATGAGAAATACATGACACTTAANAT... 572
218 GluAsnGlyArgThrPheHisLeuThrArgThrIleThrValLysValVa 234
573 ...GAAGGAAAACTT...GTAAAGCAACAACTGAATGAAAGTTAC 613
234 IglYserProLysAsnAlaValPro...ProValIleHisSerProAsn 250
614 AGCTTACTACAGACAGACCTCCCAACCACTGTTCCCATGAGAAATC 663
250 SPHisValValTyrGluLysLupProGlyGluGluLeuLeuIleProCys 266
664 AGCCAGATATATAGATGTCCAGCTGAGCTGATCAATCCCTGC 713
267 ThrValTyrPheSerPheLeuMetAspSerArgAsnGluValIlePrtPth 283
714 AAGCATCTTCGGATTCAGTGAAGCTGTGGCAATGATCACTACTG... 761
283 rIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsn 300
762 .ATGAAGAGAAAG...TTTATGAG 786
300 IuSerIleSerHisSerArgThrGluAspGluThrArg... 312
787 AACTGGCAGTCACATTAGA...GAAGGTGAATAGAGCTTCTCAAGAG 833
313 .....ThrGlnIleLeuSerIleLysValTh 322
834 CATCTGGAGAAAGAAAGATTGAATGGCACTCATCTTGACTGATGTGT 883
322 rSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysG 339
884 GGAAGCTGACCTG...GCGAATATACCTGCGCATGTTGAACCGAATG 930
339 LysIleValAlaLysAlaLysValLysGlnLys 350
931 GACGGAACATGCCAGTGTGTTGCTGCGTAAAG 965

seq_name: /sids1/gc9data/geneseq/geneseqn-emb1/NA2000.DAT:AAA27919
seq_documentation_block:
ID AAA27919 standard: cDNA: 2091 BP.
XX
AC AAA27919;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human Xrec2 cDNA coding region.
XX
KW Xrec2; Interleukin-1 receptor; X chromosome; gene therapy;
KW retinosis; lissencephaly; subcortical laminarheteropia;
KW mental retardation; chowchock syndrome; bazex syndrome;
KW hypertichosis; lymphoproliferative syndrome; immunodeficiency; ss.
OS Homo sapiens.
XX
PN WO200036108-A2.
XX
PD 22-JUN-2000.

```

```

XX
PF 14-DEC-1999; 99WO-US29549.
XX
PR 14-DEC-1998; 98US-0112163.
XX
PR 10-NOV-1999; 99US-0164675.
XX
PA (IMM) IMMUNE CORP.
XX
PI Stims JE, Smith DE, Born TL;
XX
DR WPI: 2000-442387/38.
XX
DR P-PSDB: AAY95298.
XX
PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus
XX
PS Claim 12(a); Page 8-9; 87pp; English.
XX
CC The present sequence is that of the coding region of cDNA encoding
CC human Xrec2, a member of the interleukin-1 (IL-1) receptor family
CC that is encoded by a gene on the X chromosome. The sequence was
CC obtained by high-throughput sequencing of chromosome region Xp11,
CC PCR and 5' RACE reactions. The invention is directed to novel,
CC purified and isolated IL-1 zeta, IL-1 zeta splice variants and
CC Xrec2 polypeptides (see AAY95297-301), the nucleic acids (see
CC AAA27918-22) encoding such polypeptides, processes for production of
CC recombinant forms of such polypeptides, and their uses. Xrec2
CC nucleic acids are used to: to express Xrec2 polypeptides; as probes
CC to identify nucleic acids encoding proteins of the IL-1 receptor
CC family; to identify human chromosome X; to map genes on chromosome
CC X; to identify genes associated with diseases, syndromes, or other
CC conditions associated with chromosome X, such as retinosis,
CC lissencephaly, subcortical laminarheteropia, mental retardation,
CC chowchock syndrome, bazex syndrome, hypertichosis,
CC lymphoproliferative syndrome and immunodeficiency; as
CC single-stranded sense or antisense oligonucleotides to inhibit
CC expression of Xrec2 polypeptides; to help detect defective genes in
CC an individual; and for gene therapy.
XX
SQ Sequence 2091 BP; 644 A; 432 C; 479 G; 536 T; 0 other;

alignment_scores:
Quality: 416.50 Length: 353
Ratio: 1.965 Gaps: 12
Percent Similarity: 60.057 Percent Identity: 30.312

alignment_block:
US-08-917-710-2 x AAA27919 ..
Align seg 1/1 to: AAA27919 from: 1 to: 2091

1 MetThrLeuLeuTyrPcysValValSerLeuTyrPheTyrGlyIleLeuG1 17
::: |||||:::::: |||||:::
22 TTGATTCCTCTATACGCTACTTTTACTCAGAGTTTGAAGTTGTATACCA 71
17 nSerAspAlaSerGluArgCysAspAspTyrPcylLeuAspThrMetArg 34
72 AAGAGCTCCGCCGATGATGCATGCTGCTATCAT...ATCAAGA 118
34 InIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
::: |||||::: |||||::: |||||::: |||||:::
119 AATATCAAAATTTTGGTGGAGAGCCTGTTCGATCAATCAATGTCACTTT 168
51 GluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuTh 67
::: |||||::: |||||::: |||||::: |||||:::
169 TATGTTATATCAGAAACAATTAATCTCTTGCCCAAGTCTGAGCTAG 218
67 rLeuIleTyrPyrThrThrGluAspArgAspLeuGluProIleA 84
::: |||||::: |||||::: |||||::: |||||:::
219 TTGATGTGTGACAAAGTTCTGCTGAGACTTTGAAGGCCCAATG 268

```



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532 TTGATCTCTTATACGCTACTTTACTCAGAGTTTGAGGTTGTGACCA 581
17 nseraspalasergluargcysaspasprprrglyleuasprrmetarg 34
582 AAGAGGCTCGCCGATGATGACGCTGCTATGCAAT...ATCACA 628
34 lnlleuvalpnegluasgluproalargllelscysproleupe 50
629 AATATCAAGTTTGGTGGAGAGCCGCTGCATCAATCAATGCTACTCTT 678
51 gluhispheleuyspheasntyrserthrallahiseralaglyleuth 67
679 TATGCTTAATCAACAATAATCTCTCCCTGCCAAGTGTGCACTGAG 728
67 rleuiletprrtyrthrlysglnasprargsprrleugluprrllea 84
729 TTTGATGTGTACAAAAGTTCTGCTCGAGACTTTGAGAGCCAAATG 778
84 snpheargleuprogluasargleserlysglulysaspvalleutr 100
779 CCTT...GACGAGTAGATAGAGCAAGAAGAGACTCCATTGG 822
101 pheargprothrleuleuasnasphthrgllyantyrthrlysmetleutr 117
823 TTCGCGCCACATCTCTACGAGAGAGTGTCTACGCTGTGTCATGAG 872
117 gsnthrthrtyrcysserlyvalalaphproleugluvalalaglnl 134
873 AATCTCACTTACTGTATGAAGTATCCATCTCATGACAGGGGTGAAA 922
134 ysaspsr...cyspheasnsrprometllyleuprovalhislys 148
923 ATGACACTGACTCTGCTATATTCCAAGATGAG... 957
149 leutyrileglutrygly...lleuaglyleuthcyspr 161
958 ...TATTTGAAAAGCTGACTTGCACAAACCAAGAAATTCCTGCGC 1004
161 oasnvalaspltyrphrprosersevallysprrhrlethrpt 178
1005 TGACATAGAGGATTTTCTACTGCCAACAGAACCTGAATCCTTGGT 1054
178 yrmecglycystyrlyslleuasnphnasnvalilleproglgly 194
1055 ACAAGGAATGCGAGCAAAAACATGAGGCCAAGTATGTATTCAAAAGA 1104
195 metaenleuserpheleuilealaleuilleserasnanglyasntyrth 211
1105 GATACTCTGCTTATAGAGAGCTCAGAGAACATGACATTGAAATTATAC 1154
211 rcysvalvalthrtyrprogluasnglyargthrphhisleuthrargt 228
1155 CTGTGAATTAATAAT...GGAGGCTTGTGTGAGAGAACTACTG 1198
228 hrleuthvallyvalvalglyserprolysasnalaalaproval 244
1199 AATTACTGTACA...GCCCTCTGACTGATTAACCCACCAAG 1239
245 llehisserproasnasphehis...valaltyrglulysgluprogl 259
1240 CTTTGTATCTTATGAAAGTAAGTACATTCAGAGAGCCAGCTGGG 1299
259 yglugluleuileperocysrthrvaltyrphaserpheleumetlasp 276
1290 TGACTCTGCTTATCTACTACCTGACAGCTTCTTGGTACAGCGAGATG 1339
276 erargasngluvaltrprrhrleasplglyslysprraspslle 292
1340 TCAGTCCCTTAATTACTGAGTGAAGAGAAATTTATGAGACTG 1389
293 ...thrileasvalthrleasnngluserlase 303
1390 GATGAAATGAGTGTGGAAAGTACATTAGATT...CTTA 1430

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303 hisserargthrgluasplurthrargthrlnlleuserlleysl 320
1431 GGACATCTTGGGAGCAAGAAAGTTTCATCTCATTTAAT...GTGACT 1477
320 ysalthrsergluaspleuysargserlyrvalcysghsalargser 336
1478 CTGTGGAAGAAAGTGACTTG...GGAATATTAATCTCTTATGTGAAAT 1524
337 Alarysly 339
1525 GGAATGCA 1533

seq_name: /STDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABA09029
seq_documentation_block:
ID ABA09029 standard; cDNA; 3120 BP.
AC ABA09029;
XX
XX 11-JAN-2002 (first entry)
DE Human oligophrenin-4 homologue-encoding cDNA, SEQ ID NO:805.
XX
XX Human: cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemokinesis; chemokinesis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antilucer; ss.
XX
OS Homo sapiens.
XX
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-457740/49.
XX
XX P-PSDB: ABB11785.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
XX treating or ameliorating a medical condition in a mammalian subject
XX e.g. arthritis and cancer -
XX
XX Claim 1; Page 712-713; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides,
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell

```

CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibitor-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention.

XX  
 Sequence 3120 BP; 913 A; 632 C; 680 G; 895 T; 0 other;

alignment\_scores:  
 Quality: 409.50 Length: 351  
 Ratio: 1.905 Gaps: 12  
 Percent Similarity: 61.254 Percent Identity: 30.484

alignment\_block:  
 US-08-917-710-2 x ABA09029 ..

Align seg 1/1 to: ABA09029 from: 1 to: 3120

1 MethrleuLeuTrpCysValAlaSerLeuTrpPheTrpGlyLeuGlu 17  
 532 TTGATTCCTTATACGCTACTTACTCAGAGTTTGAGGTTGTGACCA 561  
 17 nSerAspAlaSerGluArgCysAspArgPyrGlyLeuAspThrMetArg 34  
 582 AAGAGGCTCCGCCGATGATGACGATGCTATCATCAT...ATCAGA 628  
 34 InileGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50  
 629 AATATCAAGTTTGTGGAGAGCCCTGTCGAATCAATGATGCACCTTT 678  
 51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeu 67  
 679 TATGCTTATATCAGACAAATTTACTCCCTTCCCAAGTCTGTGACAC 728  
 67 rLeuIleTrpTrpTrpTrpLysGlnAspArgAspLeuGluProIleA 84  
 729 TTTGATGCTGTACAAAGTTCTGCTCTGAGACTTTGAGAGGCCAATAG 778  
 84 snPheArgLeuProGluAsnArgLysSerLysGluAspValLeuTrp 100  
 779 CCTTT.....GACGGAAGTAGAATGAGCAAGAAGAAAGACTCCATTGG 822  
 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpTrpCysMetLeu 117  
 823 TTCGGCCCAACATGTCTACAGACAGGCTGTCTACGCTGTGCACAG 872  
 117 GAsnThrTrpTrpCysSerLysValAlaPheProLeuGluValValGln 134  
 873 AAACCTCCACTTACTGTATGAAGATCATCTCATCTGACAGTGGGTGAAA 922  
 134 ysAspSer.....CysPheAsnSerPrometLysLeuProValHisLys 148

seq\_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAK52925  
 seq\_documentation\_block:  
 ID AAK52925 standard; cDNA: 3120 BP.  
 AC AAK52925;  
 DT 06-NOV-2001 (first entry)  
 DE Human polynucleotide SEQ ID NO 2454.  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 OS Homo sapiens.  
 XX  
 923 ATGACACAGGACTCTGCTATATTCGAAGATGAG..... 957  
 149 LeuTrpIleGluTrpGly.....IleGlnArgIleThrCysPr 161  
 958 ...TATTTTGAAGAAAGCTGAACCTTAGCAAAAGCAAGAAATTTATGCGC 1004  
 161 GAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrp 178  
 1005 TGACCTTAGAGGATTTTCTACGCCAACAGAGAACTGAAATCTTGGT 1054  
 178 TrpMetGlyCysTrpLysIleGlnAsnPheAsnValIleProGluGly 194  
 1055 ACAAGGAATGACAGACAAACAAATGAGGCCCAATATGTTTCAAGA 1104  
 195 MetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTrp 211  
 1105 GATACCTGCTTATAGAGAACTGAGACAGATGATGAAATTTATAC 1154  
 211 rCysValAlaThrTrpProGluAsnGlyArgThrPheHisLeuThrArg 228  
 1155 CTGTGAATTAATAAT.....GGAGCTTGTGTGTGAGAGAACTACTG 1198  
 228 hLeuThrValLysValValGlySerProLysAsnAlaValProProVal 244  
 1199 AATTAACCTTTACA.....GCCCTGTGACTGATTAACCCACAG 1239  
 245 IleHisSerProAsnAspHis.....ValAlaTrpGlyLysGluProG 259  
 1240 CTTTGTATCTTATAGCAAGTAAGTACAAATTCAGAGACCCAGCTGG 1289  
 259 yGluGluLeuLeuIleProCysTrpValTrpPheSerPheLeuMetAsp 276  
 1290 TGACTCTGCTATCTTAACCTGACAGACTTCTTGTGGTACAGCGAGATG 1339  
 276 eArgAsnGluValTrpThrPheIleAspGlyLysLysProAspAspIle 292  
 1340 TCAGTCCCTTAATTTACTGATGAAGAGAAATTTATTTGAAATCTG 1369  
 293 ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThr.... 307  
 1390 GATGAAGATCGAGTTGGGAAGTGACATTAATTTCTTAAGAGCATC 1439  
 308 ....GluAspGluThrArgThrGlnIleLeuSerIleLysLysValThr 322  
 1440 TTGGGGAACGAGAGTTTCCATCTCATTAAT...GTGAGCTGTGTGAA 1486  
 323 SerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysG 339  
 1487 GAAGTGACTTG...GGAATTAATCTGTTATGTTGAAGAAATGAAATG 1533  
 339 y 339  
 1534 A 1534









51	GIUHHPhleleuLysPheasnTySerThAlaHisSerAlaGlyLeuTh	67
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67	lleuileTPrTyrrThrThryLysGlnAspArgAspLeuGluIuProIlea	84
210	TCTGATCTGATATTGGACATAGCAGGACCGGACCTTGAGGAGCCAAATTA	259
84	snpHArleuProGluasnArgIleSerLysGluAspValIleTrp	100
260	ACTTCGCGCTCCCGAGAACCGCATATGTAAGGAGAAAGATGCTGTGG	309
101	PheArGProThrIleuIleAsnAspThrGlyAsnTrpThrCysMetIleuAr	117
310	TTCCGGCCCACTCTCCATAGACACTGGCAACTATACCTGCATGTTAAG	359
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seq\_documentation\_block: 115 1080001044

Patent No. 6280955

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:  
: ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH

STATE: CALIF  
COUNTRY: USA

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; ZIP: 94010
;
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: IIS/08/991.9444

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FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,62/  
REFERENCE/DOCKET NUMBER: T97-014

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342  
INFORMATION FOR SEO ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3355 base pairs

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; TYPE: nucleic acid
STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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FEATURE:	CDS
NAME/KEY:	

LOCATION  
US-08-991-944-3

alignment\_scores:  
quality: 1660.00

ratio:	4.555	caps:	
Percent Similarity:	95.714	Percent Identity:	84.857

alignment\_block:

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1. Accounting Principles Volume 1 1st edition 2010 ISBN 978-0-13-035957-9 © 2010 Pearson Education, Inc. All rights reserved. Printed in the United States of America. 10 9 8 7 6 5 4 3 2 1

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seq_documentation_block:
; Sequence 3, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:

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```

APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
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586 GGAATGCTCTGTCATCCAAAGTTCACAGAAAGATGAGGAGAAATTA 635  
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seq_documentation_block:
Sequence 1, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: YES
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1737
; OTHER INFORMATION: /note= "splice junction"
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "splice junction"
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32 eTarGlnIleGlnValPheGluAspGluProAlaArgIleLysCysPro 48
98 TCAAGACATACATGCGCTTGGCAGGTCAACACATCCGAGTGAATGTGCC 147
49 LeuPheGluHisPheLeuLysPheAsnTySerThrAlaHisSerAlaG1 65
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82 roIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspVal 98

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286 ATATGCTTTCACCTCAGCTGAGGCAACAGACAGTGTGATTCATCAGTGTGT 335
115 tLeuArgAsnThrTrpTyCysSerLysValAlaPheProLeuGluVal 132
336 TTAAAGAACTCAACATATTCATGAAGGTGTCAATGCTTGCATCTGTG 385
132 alGlnLysAspSer.....CysPheAsnSerProMetLysLeuProVal 146
386 CAGAGAAATGAATCAGCGCTGTGCTACCAACAGCAGATCCGC..... 426
147 HisLysLeuTyrlleGluTyGly.....IleGlnArgIleThr 159
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518 TGTGCTATTAAGAAATGCAAGCCAAATGTGCAAGACATATATATACG 567
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: Patent No. 6326472
: GENERAL INFORMATION:
: APPLICANT: Timans, Jacqueline C.
: APPLICANT: Debets, Johannes Eduard Maria
: APPLICANT: Antonius
: APPLICANT: Sana, Theodore R.
: APPLICANT: Bazan, J. Fernando
: APPLICANT: Kastelein, Robert A.
: TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNA Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/173,151A
: FILING DATE: 14-OCT-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/065,776
: FILING DATE: 17-NOV-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/078,008
: FILING DATE: 12-MAR-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/081,883
: FILING DATE: 15-APR-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/095,987
: FILING DATE: 10-AUG-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/078,416
: FILING DATE: 18-MAR-1998
: APPLICATION DATA:
: APPLICATION NUMBER: US 60/062,066
: FILING DATE: 15-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0767X
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650)852-9196
: TELEFAX: (650)496-1200
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2537 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..2004
: US-09-173-151A-34

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1 APPLICANT: Cosman, David J.
2 APPLICANT: Lipton, Stephen D.
3 APPLICANT: Mosley, Bruce A.
4 APPLICANT: Dower, Steven K.
5 TITLE OF INVENTION: Type II Interleukin-1 Receptors
6 NUMBER OF SEQUENCES: 14
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Immunex Corporation
9 STREET: 51 University Street
10 CITY: Seattle
11 STATE: WA
12 COUNTRY: USA
13 ZIP: 98101
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentin Release #1.24
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US91/03478
21 FILING DATE: 19910517
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 07/534,193
25 FILING DATE: 06-JUN-1990
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/573,576
28 FILING DATE: 24-AUG-1990
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 07/627,071
31 FILING DATE: 13-DEC-1990
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Wight, Christopher L.
34 REGISTRATION NUMBER: 31680
35 REFERENCE/DOCKET NUMBER: 2003-WO
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 206-587-5570
38 TELEFAX: 206-233-0644
39 INFORMATION FOR SEQ ID NO: 12:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1366 base pairs
42 TYPE: NUCLEIC ACID
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: cDNA to mRNA
46 HYPOTHEICAL: N
47 ANTI-SENSE: N
48 ORIGINAL SOURCE:
49 ORGANISM: Mouse
50 CELL LINE: 702/3
51 IMMEDIATE SOURCE:
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55 NAME/KEY: CDS
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seq documentation block:
/ Sequence 3, Application US/08381603
/ Patent No. 5858355
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/ GENERAL INFORMATION:
/ APPLICANT: Giortoso, Joseph C.
/ APPLICANT: Evans, Christopher H.
/ APPLICANT: Robbins, Paul D.
/ TITLE OF INVENTION: Gene Transfer For Treating a C
/ TITLE OF INVENTION: Mammalian Host
/ NUMBER OF SEQUENCES: 6
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Eckert Seamans Cherin & Mellott
/ STREET: 1700 Market Street Suite 3232
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/381,603
/ FILING DATE:
/ CLASSIFICATION: 514
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gould, Jr., Lewis F.
/ REGISTRATION NUMBER: 25,057
/ REFERENCE/DOCKET NUMBER: 109070-11
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 575-6000
/ TELEFAX: (215) 575-6015
/ TELEEX: 866172
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1782 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
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/ CLONE: Mouse Interleukin-1 Receptor
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/ NAME/KEY: CDS
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364 TGCCCAAAACTAAAGTAACTGTAAGTGTGTAAGAAATGACCCCTGGCTT 413
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323 rGluAspLeuLysArgSerTyrValCys 332
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seq.name: /cgn2.6/prodata/1/lna/6A.COMB.seq:US-08-924-376-3

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seq\_documentation\_block:

Sequence 3, Application US/08924376

Patent No. 6159464

GENERAL INFORMATION:

APPLICANT: Glorioso, Joseph C.

APPLICANT: Evans, Christopher H.

APPLICANT: Robbins, Paul D.

APPLICANT: Bandera, Geethani

TITLE OF INVENTION: Gene Transfer For Treating a

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eckert Seamans Cherin & Mellott

STREET: 1700 Market Street Suite 3232

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/924,376

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/027,750

FILING DATE: 08-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gould, Jr., Lewis F.

REGISTRATION NUMBER: 25,057

REFERENCE/DOCKET NUMBER: 109070-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 575-6000

TELEFAX: (215) 575-6015

TELEX: 866172

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1782 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

LIBRARY: Mouse T-cell cDNA library

CLONE: Mouse Interleukin-1 Receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 46..1776

US-08-924-376-3

alignment\_scores:

Quality: 257.00 Length: 326  
Ratio: 1.436 Gaps: 17  
Percent Similarity: 54.908 Percent Identity: 25.767

## alignment block:

US-08-917-710-2 x US-08-924-376-3 ..

Align seg 1/1 to: US-08-924-376-3 from: 1 to: 1782

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34 GlnIleGlnValPheGluAspGluProAlaArgIle..... 45
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106 GAATTCAGCATGATGACAGAAATATCCAAATCAGATCGTTGTTGTTATC 155
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46 .....LysCysProLeuPheGluHisPheLeu 55
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156 TGTAATGAATGATGATTCGCAAGTGTCTCTACTCCAAATAAATATGC 205
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55 LysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTyr 71
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913 AAAAGAAATACACATCATTTACACACCTTACATTTTCAGAGTTAAAG 962
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323 rGluAspLeuLysArgSerTyrValCys 332
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963 CCAGTTTATGCTATCCGTTTATCTGT 990

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## seq\_documentation\_block:

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; Sequence 3, Application US/08685212
; Patent No. 6228356
; GENERAL INFORMATION:
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Evans, Christopher H.
; APPLICANT: Robbins, Paul D.
; APPLICANT: Bandara, Geethani
; TITLE OF INVENTION: Gene Transfer For Treating a
; TITLE OF INVENTION: Connective Tissue of a Mammalian Host
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,212
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/027,750
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 109070-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6000
; TELEFAX: (215) 575-6015
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Mouse T-cell cDNA library
; CLONE: Mouse Interleukin-1 Receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..1776
; US-08-685-212-3

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## alignment\_scores:

Quality: 257.00 Length: 326  
 Ratio: 1.436 Gaps: 17  
 Percent Similarity: 54.908 Percent Identity: 25.767

## alignment\_block:

US-08-917-710-2 x US-08-685-212-3 ..

Align seg 1/1 to: US-08-685-212-3 from: 1 to: 1782

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46 .....LysCysProLeuPheGluHisPheLeuL 55
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156 TGTAAATGAATGATTCGCAAGTGTCTTCTTCTCCAAATTAATAATGC 205
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122 CysSerLysValAlaPheProLeuGluValAlaGlnLysAspSer.... 136
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364 TGCCCAAACTAAAGTAAACCGTACTGTGTAGGAATGACCCGCTT 413
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201 leAlaLeuIleSer.....AsnAsnGlyAsnTyrThrCysValValThr 215
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216 TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrVal 232
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652 TATACGTTCCGGGGAAGCATATATCCGTCACACGAGTAAATACATTAT 701
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749 GGAATGAGAGATC...GAAAGTGAACCCAGATCAATGATCAACATGATC 795
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834 GAAGTGAATGATCA.....GAATTCGAATGA 862
299 snGluSer.....IleSerHisSerArgThr 307
   :::::::::::  :::::::::::
863 ATGATCCATTCTTAGCTGAAAGACATATCAATTTGTGGAACATCTTCAAC 912
308 GluAspGlu...ThrArgThrGlnIleLeuSerIleLysValThrSe 323
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seq_name: /cgn2_6/prodata/1/lna/PCTUS_COMB.seq:PCT-US94-02414-3
seq_documentation_block:
; Sequence 3, Application PC/TUS9402414
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh of the Commonwealth System of Higher Education
; TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue Disorder
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02414
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 109070-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6000
; TELEFAX: (215) 575-6015
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Mouse T-cell cDNA Library
; CLONE: Mouse Interleukin-1 Receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..1776
; PCT-US94-02414-3

alignment_scores:
Quality: 257.00 Length: 326
Ratio: 1.436 Gaps: 17
Percent Similarity: 54.908 Percent Identity: 25.767

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alignment\_block:  
US-08-917-710-2 x PCT-US94-02414-3 ..

Align seg 1/1 to: PCT-US94-02414-3 from: 1 to: 1782

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156 TGTAAATGAATGATATTCGCAAGTCTCTCTACTCCAAATTAAT 205
55 yspheasnYrSerThrAlaHisSerAlaGlyLeuThrleuLeuTyr 71
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264 GGAATCCAGATTCATCAGCAGATGAACATCTTTGTTGTTACCGCA 313
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122 CysSerLysValAlaPheProLeuGluValAlaGlnLysAspSer.... 136
364 TGCCCTCAAACTAAGTAACCGTAACGTGTAGAGAAATACCCCTGCT 413
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414 GTGTTACAGCACACAGCCACCTTCCCA...CAGCGCTCCACATGACC 459
153 YrGlyIleGlnArgIleThrCysProAsnValAspGlyTrpPhe..... 167
460 ..GGGAGTGAAGCTGTGTGGCCCTATATG..AGTTATTTTAAAGAT 504
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834 GAAGTGAATGATGATCA.....GAAATGAAGAAGA 862

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299 snGluSer.....IleSerHisSerArgThr 307
863 ATGATCCATTCTTAGCTGAGACACTATCAATTTGGAAACATCTTCAAC 912
308 GluAspGlu...ThrArgThrGlnIleLeuSerIleLysValThrSe 323
913 AAAGAANAATACACCTCATATACAACTTACATTTACAGAAATTAAAG 962
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seq\_name: /cgn2\_6/prodata/1/lna/PCTUS\_COMB.seq:PCT-US96-08899-3

seq\_documentation\_block:

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? Sequence 3, Application PC/TUS9608899
? GENERAL INFORMATION:
? APPLICANT: University of Pittsburgh of the Commonwealth
? TITLE OF INVENTION: System of Higher Education
? TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of a
? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Eckert Seamans Cherin & Mellott
? STREET: 1700 Market Street Suite 3232
? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19103
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US96/08899
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gould, Jr., Lewis F.
? REGISTRATION NUMBER: 25,057
? REFERENCE/DOCKET NUMBER: 109070-12A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 575-6000
? TELEFAX: (215) 575-6015
? TELEX: 866172
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1782 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? IMMEDIATE SOURCE:
? LIBRARY: Mouse T-cell cDNA Library
? CLONE: Mouse Interleukin-1 Receptor
? NAME/KEY: CDS
? LOCATION: 46..1776
? PCT-US96-08899-3

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alignment\_scores:

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Quality: 257.00 Length: 326
Ratio: 1.436 Gaps: 17
Percent Similarity: 54.908 Percent Identity: 25.767

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alignment\_block:  
US-08-917-710-2 x PCT-US96-08899-3 ..

LOCATION: 225...





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SEQUENCE CHARACTERISTICS:
LENGTH: 1357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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HYPOTHEetical: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Human B cell lymphoblastoid
CELL LINE: CB23
IMMEDIATE SOURCE:
LIBRARY: CB23 cDNA
CLONE: PHIL-1R175
FEATURE:
NAME/KEY: CDS
LOCATION: 154..1350
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
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NAME/KEY: sig_peptide
LOCATION: 154..192
OTHER INFORMATION:
US-08-091-519-1

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Ratio: 1.383 Gaps: 13
Percent Similarity: 54.142 Percent Identity: 23.373

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alignment_block:
US-08-917-710-2 x US-08-091-519-1 ..

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Align seg 1/1 to: US-08-091-519-1 from: 1 to: 1357

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604 GATGCCCTGACCTGAGTGAATTCACCCGTCACAAATGACGTAAGAT 653
175 eThrTrpTyrMetGlyCysTyrLysIleGlnAspPheAsnValIleP 192
||| |||||:|||||:|||||:|||||:|||||:|||||:
654 TCAATGTACAAAGATCTCTCTTTTGGATTAAGACATAGAAATTC 703
192 roGluGlyMetAsnLeuSerPheLeuIle.....AlaLeuIleSer 205
704 TAAAGTGAGGGGAGCACCTCACTTACTGTACAGATGTGGCCCTGGAA 753
206 AsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGlyArgTh 222
::: ||| |||||:|||||:|||||:|||||:|||||:|||||:
754 GATGCTGGCTATTACCGCTGTCTCTGACATTTGCCATGAAGGCCAGCA 803
222 rPheHisLeuThrArgThrLeuThrValLysValValGlySerProLys 239
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
804 ATACACATCACTAGAGATGTAGCTACGCAATCAAGAAAAAAGAG 853
239 snAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
854 AGACCAAT...CTGTGATCATTTCCCTCAAGACCAATA.....TCA 894
256 LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPh 272
::: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
895 GCTTCTGTGGGGTCAAGACTGACATCCCTGTAGGTGTTCTGGGAAC 944
272 eLeuMetAspSerArgAsnGluValTyrTrpThrIleAspGlyLysLysP 289
::: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
945 CGGCACACCTTAACACACATGCTGTGTGAGCGGCAAT..... 984
289 roAspAspIleThrIleAspValThrIleAsnGluSerIleSerHisSer 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
985 .....GACACCCCATTAAGAGCGCCCTCAACCGGAGGCG 1017
306 ArgThrGluAspGluThrArgThrGlnIle..... 315
1018 CGCGTGACGAGGGGCCAGCCAGATATTCAGAAATATATAGAACTA 1067
316 .....LeuSerIleLysLysValThrSerGluAspLeuLysA 328
1068 CATTAAGTGCATTTGATTTGATCTGTGACACAGAGAGATTTGCACA 1117
328 rGserTyrValCys 332
:::|||||:|||||:|||||:|||||:|||||:|||||:
1118 TGGATTTTAAATGT 1131

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OM of: US-08-917-710-2 to: EST.\* out-format: pfs  
 Date: Jun 11, 2002 11:09 PM  
 About: Results were produced by the Gencore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=firmat-p2n.model -DEV=xlh  
 -O/cgnt2.1/USPTO.spool/US0891710/runat.11062002.151026.18676/app-query.fasta.1.417  
 -DB=EST -OEMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000  
 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500  
 -GAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000  
 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
 -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0  
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEASize=500  
 -MINLEN=0 -MAXLEN=200000000 -USER=US0891710.0@CN1.1.6249  
 -NCP=6 -ICP=3 -LONGLOG -DEV=TIMEOUT=120 -WARN\_TIMEOUT=30  
 -NO\_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-08-917-710-2  
 Query length: 356  
 Database: EST.\*  
 Database sequences: 13736207  
 Database length: -1841457050  
 Search time (sec): 1690.340000

Score\_list:

Sequence	Strd Orig	ZScore	EScore Len	Documentation
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gb_est1:BB862501	1292.00	2721.29	2.5e-142	873
gb_est1:AL543511	1286.00	2708.86	1.2e-141	849
gb_est1:BI330085	1274.00	2682.88	3.4e-140	880
gb_est1:BI331848	996.00	2092.98	4.9e-107	756
gb_est1:AV656295	937.00	2069.74	4.9e-106	888
gb_est1:BB862523	937.00	1970.27	1.7e-100	596
gb_est1:AV659167	924.00	1937.47	1.1e-98	910
gb_est1:AA237107	900.00	1888.11	6.4e-96	789
gb_est1:BB625831	870.00	1828.68	1.3e-92	598
gb_est1:AA237486	855.00	1794.64	1.0e-90	552
gb_est1:BB626271	830.00	1786.44	2.9e-90	533
gb_est1:BB626271	831.00	1743.72	7.0e-88	643
gb_est1:AA107535	814.00	1707.11	7.3e-88	676
gb_est1:AA107535	814.00	1707.11	7.3e-88	676
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gb_est1:BB612046	802.00	1681.94	1.9e-84	646
gb_est1:AL544533	781.00	1632.91	1.0e-81	923
gb_est1:AV661936	776.00	1627.17	1.2e-81	616
gb_est1:AA571281	769.00	1614.80	1.1e-80	500
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gb_est1:BB633613	684.00	1432.82	1.5e-70	545
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gb_est1:BG711109	587.00	1258.47	7.5e-61	586
gb_est1:AV654169	566.00	1176.27	2.4e-59	335
gb_est1:BI872969	566.00	1176.27	2.4e-59	335
gb_est1:BB633613	497.50	1035.30	2.0e-48	570
gb_est1:BB633613	496.50	1036.70	2.0e-48	570
gb_est1:BB633613	494.50	1029.13	4.5e-48	560
gb_est1:BB633613	491.00	1025.88	6.8e-48	396
gb_est1:BB633613	490.00	1020.45	1.4e-47	520
gb_est1:BB644209	463.00	985.71	1.5e-44	415
gb_est1:BB644209	463.00	985.71	1.5e-44	415
gb_est1:BB644209	442.00	963.81	2.6e-38	547
gb_est1:BB644209	409.00	853.81	5.3e-38	513
gb_est1:BB644209	394.50	823.47	1.3e-36	309
gb_est1:BB644209	380.00	796.84	3.9e-35	218
gb_est1:BB644209	372.00	779.86	3.4e-34	217
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 DEFINITION Homo sapiens, interleukin 1 receptor accessory protein, clone IMAGE:3920152, mRNA.  
 ACCESSION BC016141.1 GI:16359373  
 VERSION  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1549)

late

REFERENCE  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
 COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC/DCMP/DRP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada  
 Info@gscc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Ulisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
 Series: IRAC Plate: 15 Row: 1 Column: 7  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504660  
 This clone has the following problem: frame shifted.

FEATURES  
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 /db\_xref="Locustid:3556"  
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 /clone="IMAGE:3920152"  
 /tissue\_type="Skin, melanotic melanoma."  
 /clone\_id="NIH\_MGC\_72"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SportC"

BASE COUNT  
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 480 a 340 c 331 g 398 t

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 Percent Similarity: 99.719 Percent Identity: 99.438

alignment\_block:  
 US-08-917-710-2 x BC016141  
 Align seg 1/1 to: BC016141 from: 1 to: 1549

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206 ATGACACTTCTGTGTGTAGTGAAGTCTTCTACTTTTATGGAATCTCTGA 255
17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34
|||||
256 AAGTATGCTCTCAGAACGCTGCATGACTGGGACTAGACACCATGAGGCG 305
34 InIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
|||||
306 AATTCAGAGTTTGAAGATGAGCCAGCTCCGATCAAGTCCACACTCTTT 355
51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeuPhe 67
|||||
356 GAACACTTCTTGAAATTCACACTACACACACACCCATTCAGTGGCTTAC 405
67 rLeuIleTrpTrpTrpThrLysGlnAspArgAspLeuGluProIleA 84
|||||
406 TCTGATCTGTATTTGACTAGGACGAGGACCTTGAGGAGCCAAATTA 455
84 snrPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
|||||
456 ACTTCGGCCCTCCCGAGAACCCGATTAGTAAAGAAAGATGTGTGG 505
101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuArg 117
|||||
506 TTCCGGGCCCTCTCCCAATGACACTGCGCACTATACCTGCTGTTAAG 555
117 gasnThrThrTrpCysSerLysValAlaPheProLeuGluValValGlnI 134
|||||
556 GAACACTACATATTTGACGAAAGTGCATTTCCCTTGGAAGTTGTTCAA 605
134 yAspSerCysPheAsnSerPrometLysLeuProValHisLysLeuTrp 150
|||||
606 AAGCACCCTGTTCAATCCCATGAACTCCAGTGCATTAACGTAT 655
151 IleGluTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTrp 167
|||||
656 ATAGAAATATGTCATTCAGAGATCAGTGTGCCAATGTATAGATGATTT 705
167 eProSerValLysProThrIleThrTrpTrpMetGlyCysTrpLysI 184
|||||
706 TCTTCCAGTGTCAAAACCGACTATCCTGTATATGGCTGTATATAAAA 755
184 IeGlnAsnPheAsnValIleProGluGluMetAsnLeuSerPheLeu 200
|||||
756 TACGAATTTTAAATATGATATACCGAAGGATGAACCTTGAGTTCTTC 805
201 IleAlaLeuIleSerAsnAsnGlyAsnTrpThrCysValValThrTrp 217
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806 ATTGCCTTAATTTCAATTAATGAAATTACACATGTTGTTACATATCC 855
217 oGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234
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856 AGAAAGAGGAGTACGTTTCATCTCACAGACCTGACGTGTAAAGGTAG 905
234 alGlySerProLysAsnAlaValProProValIleHisSerProAsp 250
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906 TAGGCTCTCCAAAATGACAGTGCCTCTGATCCATTCACCTTAATGAT 955
251 HisValValTrpGluLysGluProGluGluLeuLeuLeuProCysTh 267
|||||
956 CATGGGCTCTAGAGAAAGAACGAGAGAGAGTACTCATTTCCCTGTAC 1005
267 rValTrpPheSerPheLeuMetAspSerArgAsnGluValTrpTrp 284
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1006 GGTCTATTTAGTTTCTGATGATTCCTCCCAATGAGGTTGGTGAGCA 1055
284 IeAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
|||||
1056 TTGATGAGAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 1105

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1106 GT.ATAAGTCTACTATACAGAAAGATGAAACAAAGCAATGATTTGAG 1154
317 rIleLysLysValThrSerGluAspLeuLysArgSerTrpValCysHis 334
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1155 CATCAAGAAAGTTACTCTGAGATCTCAAGCCGACGCTATGTGTCATG 1204
334 IaArgSerAlaLysGlyValAlaLysAlaAlaLysValLysGlnLys 350
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1205 CTAGAGTGGCCAAAGGCGCAAGTTCCTCAAGAGCGCAAGGTAAGCAAAA 1254
351 GlyAsnArgCysGlyGln 356
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1255 GGTATATGATCGCGTCAG 1272
seq_name: gb_est2:BI862501

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DEFINITION 603390624F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3399668 5',
            mRNA sequence.
ACCESSION  BI862501
VERSION    BI862501.1 GI:16003248
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 873)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: DCTD/DRP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://lham12018.row.p column: 05
            plate: lham12018 row: p column: 05
            High quality sequence stop: 838.
            Location/Qualifiers
                1..873
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5399668"
                /clone_1kb="NIH_MGC_87"
                /tissue_type="mammary adenocarcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: breast; Vector: pCMV-Sport6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
                Average insert size 1.383 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC library."

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FEATURES
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alignment_block:
US-08-917-710-2 x BI862501 ..

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Align seg 1/1 to: BI862501 from: 1 to: 873

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91 ArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAs 107
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107	nAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSerL	124
51	TGCACTGGCGAACTATACCTGCATGTGTAAGAACACTACATATTGGACA	100
124	ySAlaIaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
101	AMSTCCATTTCCCTTGGAAAGT. GTTCAAAAAGACAGCTGTTCAATTCC	149
141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnAr	157
150	CCCATGAACCTCCCACTGCATATAACCTGTAATGAAATATGGCACTTACAG	199
157	gIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProT	174
200	GATCACTTCTCCAAATGTAGATGGAATATTCTTCCTCCAGTGCACAAACGA	249
174	hIleThrTrpIleMetGlyCysTyrLysIleGlnAsnPheAsnVal	190
250	CTATCACTTGGTAATAGGGCTGTAAATAACAGAAATTTATATATGTAA	299
191	IleProGluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAs	207
300	ATACCCGAAGATGATGACTGATGTTTCCCATTCGCTTAATTCCAAATTA	349
207	nGlyAsnTyrThrCysValValThrTyrProGluAsnGlyArgThrPhe	224
350	TGGAAATTAACACATGTGTGTGTACATATCCCAAAATGAGACGTACGTTTC	399
224	IleLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
400	ATCTACACGAGCACTGTACTGTAAAGTAGTAGGCTCTCCCAAAAATGCA	449
241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysG	257
450	GTGCCCTCTGATCCATTCACCTAATATATCATGTGGCTATGAGAAACA	499
257	nProGlyLeuGluLeuLeuIleProCysThrValTyrPheSerPheLeu	274
500	ACCAGAGAGAGAGCTACATCATCTCCCTGTACGGCTCAATTTAATTTTCA	549
274	eAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAsp	290
550	TGGAATTCGCAATAGAGTTGGTGGACCAATTGATGAGAAAAAACCTGAT	599
291	AspIleThrIle. AspValThrIleAsnGluSerIleSerHisSerArgT	307
600	GACATCACTAATGTGATGTCCACCATTAAACGAAAGTAATGATCATAGTACA	649
307	hArgLysAspGlu. ThrArgThrGlnIle. LeuSerIleLys. LysValThr	322
650	CAGAGAGTGAAGAAACACAGAACTCAGATTTTATAGCTACAGAAAGTTACC	699
323	SerGluAspLeuLysArgSerTyrValCysHisAlaArg. SerAlaLysG	339
700	TCTAGAGATCTCAAGCGCAGCTATGTCTGTATGCTAGTAAAGGCTGCCAAG	749
339	LysIleVal. AlaLysAlaAlaLysValLysGlnLysGlyAsn. ArgCys	354
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seq_documentation_block:
  docu: 174354
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DEFINITION	AL543511 LTT1_NFL006_P12	Homo sapiens	cDNA clone	CS0D1003YK15	5
ACCESSION	AL543511	prime, mRNA sequence.			

VERSION	AL543511.1	GI:12875989
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 849)	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Genoscope	
	Genoscope - Centre National de Sequencage	
	BP 191 91006 EVRY cedex - France	
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	
FEATURES	Location/Qualifiers	
SOURCE	1. 849	

	http://fulllength.invitrogen.com"				
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ORIGIN					

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    Ratio: 5.336
Percent Similarity: 97.571
Percent Identity: 95.951
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alignment_block:
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US-08-917-710-2 x AL543511

Align seg 1/1 to: AL543511 from: 1 to: 849

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17 nSeraspAlaSerGluAlaGlyCysaspApPTpClyLeuaspHrMetArg 34  
160 AAGTGAATGCTCTCAGAACGCTCGAGATGACTGGGAGACTAGACACATGAGGC 209  
34 InIleGlnValPheGluaspGluProAlaArgIleLysCysProLeuPhe 50  
210 AAATTCACAAGTGTGAGATGAGCCAGCTCGCATCAATGCCCACCTCTT 259  
51 GluHisPheLeuLysPheAsnYrSerThrAlaHisSerAlaGlyLeu 67  
260 GAACACTCTGTGAATTCACATCACAGCCAGCCCATTCAGCTGCCTTAC 309  
67 rLeuIleLeuPyrTrpThrLysGlnaspArgAspLeuGluProIle 84  
310 TCTGATCTGGTATTGTGACTAGCAGCAGCCGGACCTTGAGAGGCCAATTA 359  
84 snPheArgLeuProGluAsnArgIleSerLysGluLysaspValLeuTrp 100  
360 ACTTCGCGCTCCCCGAGAACCCGCAATTAAGTAGGAGAAAGATGTCCTGTGG 409  
101 PheArgProThrLeuAsnAspHrClyAsnYrThrCysMetLeu 117  
410 TTCGGGCCACACTCTCTCAATATGACTGGCAACTATACCTGCAGATTAG 459



\_\_\_\_\_

100

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 888)  
TITLE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9abs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LRAM1332 row: h column: 08  
High quality sequence stop: 802.

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/strain="FVB/N"  
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/clone="IMAGE:5135287"  
/lab\_host="NCI CGAP L19"  
/note="Organ: Liver; Vector: pCMV-Sport6; Site\_1: NCI;  
Site\_2: Salt; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP Library."

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ORIGIN

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Percent Similarity: 91.020 Percent Identity: 79.592

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US-08-917-710-2 x B1331848 ..

Align seg 1/1 to: B1331848 from: 1 to: 888

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17 nSerAspAlaSerGluArgCysAspArgPrgIleuAspPthMetArg 34
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
170 GAGTCATGCTTCGAGCGCTGTGATGACTGGAGCTAGATACCATCGAC 219
34 IntIleGlnValPheGluAspGluProIleArgIleLeuCysProLeuPhe 50
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 AAATCCAGGTGTTGAAGATGAGCGGCTGAAATCAAGTCCCCCTTT 269
51 GluHisPheLeuLysPheAsnTySerThrAlaHisSerAlaGlyLeuTh 67
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
270 GAACATCTCCGAGAGTACACTACAGCAGCCTCATCTGCGCTTAC 319
67 rLeuIleTrpTyTrpThrIysGlnAspArgAspLeuGluProIleA 84
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320 CCTATCTGTGATCGACCAAGACCGGAGCTGTGAGAGCCCATTA 369
84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
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370 ACTTCCGCTCTCCAGAGATGCGATCAGTAAGGAGAAAGTGTCTGTG 419
101 PheArgProThrIleuLeuAsnAspPthGlyAsnTyThrCysMetLeuAr 117
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420 TTCGGGCGCCACCTCCTCATGACAGGCGCAATTAACCTGCATGTGAG 469
117 gAsnThrThrTyCysSerLysValAlaPheProLeuGluValAlaGln 134

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470 GACACACTTACTGCAGCAAGTTGATTTCCCGGAAGTTGCAG 519
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
134 ysAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTy 150
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520 AGCAGACTGTTCATTCATTCGATGAGATTCCTCAGTGCACAGAGTAT 569
151 IleGluTyArgIleGlnArgIleThrCysProAsnValAspGlyTyP 167
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570 ATGAAATGCGATCATTAAGATCATGTCACAAATGTGACGATAC 619
167 heProSerValLysProThrIleThrTrpTyMetGlyCysTyLys 183
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620 TTCCTTCAGTGCATCAACCATCGGTCTGTATTAAGGTTGTACTGAA 669
184 IleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPhe 200
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
670 ATAGTGCATCTCATAAATGATCCAGGAGCATGAACTGAGCTTTTC 717
200 uIleAlaLeuIleSerAsnAsnGlyAsnTyThrCysValValThr...T 216
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718 ATCCCTGTGTTTCATACATACAGSAACTACACATGTGTGTTACCAT 766
216 yrProGluAsnGlyArgThrPheHisLeuThrArgThrIleuValLys 232
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
767 TCCTGTAAGAAAGCGGAGCGCTCTTTCACCTCACAGATGTGACTGTA 816
233 ValValGlySerProLysAsnAlaValProPro 243
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seq\_name: gb\_estl:AV656295

seq\_documentation\_block:  
LOCUS AV656295 596 bp mRNA linear EST 16-JAN-2002  
DEFINITION AV656295 GIC Homo sapiens cDNA clone GICPH02 3', mRNA sequence.  
ACCESSION AV656295  
VERSION AV656295.1 GI:9877309  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 596)  
Xiao, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
Hu, G., Gu, J., Chen, Z. and Han, Z.  
Insight into hepatocellular carcinogenesis at transcriptome level  
by comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
21625106  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
Source  
1..596  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GICPH02"  
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BASE COUNT 201 a 111 c 125 g 159 t



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Quality: 937.00 Length: 177  
Ratio: 5.294 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 99.435

## alignment\_block:

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Align seg 1/1 to: AV656295 from: 1 to: 596

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196 nleuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysV 213
|||||
60 CTGAGTTTCTCATTCCTTAATTTCAAAATATGGAATTAACACATGTG 109
|||||
213 AlValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeu 229
|||||
110 TTGTACATATCCAGAAATGAGCTACCTTTCATCTCACAGGACTGTG 159
|||||
230 ThrValLysValAlaGlySerProLysAsnAlaValProValIleHis 246
|||||
160 ACTGTAAGGTAGTAGCTCTCCAAAATAATGACAGTCCCTGTGATCCA 209
|||||
246 sSerProAsnAspHisValValTyrGluLysGluProGlyGluLeuL 263
|||||
210 TTCACCTATATGATCATGTGTCTATGAGAAAGAACAGAGAGAGCTAC 259
|||||
263 euIleProCysThrValTyrPheSerPheLeuMetAsSerArgAsnGlu 279
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260 TCATTCCTGTACGGTCTATTGTTTCTTGATGATGATTCGCAATGAG 309
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280 ValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspVa 296
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310 GTTGGTGAGCATTGATGAGAAAAAACCTGATGACATCACTATTGATGT 359
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296 lThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgT 313
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360 CACCATTAACGAAAGTATTAAGTCTATAGAGAACAGAAAGATGAACAAGAA 409
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313 hIleGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSer 329
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410 CTCAGATTTTGAGCATCAAGAAAGTTAAGTCTGAGATCTCAAGCGCAGC 459
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330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLys 346
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460 TATGTCTGTCTATGCTAGAGAGTCCAAAGGGCAAAATTCGCAAGACGCAAA 509
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346 sValLysGlnLysGlyAsnArgCysGlyGln 356
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510 GGTGAACAGAAAGTATATAGATGCGGTGAG 540
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DEFINITION 601435065P1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920152 5',
mRNA sequence.
ACCESSION BE892231
VERSION BE892231.1 GI:10352355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

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## JOURNAL COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC/DC/DTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed, by: The I.M.A.G.E. Consortium (ILLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILLN at:  
http://image.llnl.gov  
Plate: LLAM9751 row: a column: 17  
High quality sequence stop: 710.

## FEATURES

## source

Location/Qualifiers

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/organism="Homo sapiens"  
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/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; Ncti:  
Site\_2: Salt; Cloned unidirectionally. Primer: oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

BASE COUNT 236 a 241 c 210 g 223 t

## ORIGIN

## alignment\_scores:

Quality: 924.00 Length: 249  
Ratio: 4.667 Gaps: 4  
Percent Similarity: 79.518 Percent Identity: 76.305

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US-08-917-710-2 x BE892231 ..

Align seg 1/1 to: BE892231 from: 1 to: 910

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|||||
17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspTrpMetArgG 34
|||||
233 AATGATGCTTCAGAACCGCTGCCATGCTGGGAGTACAGACCATGAGAGC 282
|||||
34 lIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
|||||
283 AAATCCAAAGTGTGAAAGATGAGCCAGCTCGCATCAAGTCCGACTCTTT 332
|||||
51 GluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuTh 67
|||||
333 GAACACTTCTTGAATTAACATACACACAGCCCAATTCAGTGGGCTTAC 382
|||||
67 lleuIleTrpTyrTrpThrLysGlnAspArgAspLeuGluIuproIleA 84
|||||
383 TCGATCTGTGATTTGAGTACGACAGACCGGACCTTGAGGAGCCAAATTA 432
|||||
84 snPheArgLeuProGluAsnArgIleSerLysGlnLysAspValLeuTrp 100
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433 ACTTCCGCGCTCCCGAGAACCCGATTAAGAGAGAAAGATGTGCTGAG 482
|||||
101 PheArgProThrLeuLeuAsnAspPheArgLysAsnTyrThrCysMetLeuAr 117
|||||
483 TTCGGGCCACCTCTCCATATGACATGCAACATTAATCTGCATGTTAG 532
|||||
117 gAsnThrThrTyrCysSerLysValAlaAlaPheProLeuGluValGlnL 134
|||||
533 GAACACTACATATTGCAGCAAGTT.GCATTTCCCTTGGAATGTTTCAA 581
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134 yAspSerCysPhe AsnSerProMetLysLeuProValHisLysLeuT 150
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582 AAGACAGCTGTTCAAATTCGCCCATGAAGTCCCAAGTGCATTAACCTGT 631

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150 yrllelglutyr. Glylileglarlgilethrcysproasnvalasgltyr 166  
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 166 rhpheproserVallyserProthrllethrtprlymetglcysTyrL 183  
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 682 TTTTCTTCAGAGT. AAACGACATCATCTGTTATATGGCTTATRA 730  
 183 yslllelnasnpheasnvalilleprogluglymetasnleuserphe 199  
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 731 AATACGACATTC..... 744  
 200 leuilealelleuleserasnnglyasnrythrncysvalallethrt 216  
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 216 rprogluansgllyargthrphethrleuthrargthrleuthrvallysv 233  
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 753 TACCGAAGTTGACCTGATTCGATCCCTTAATGACCTTATGATTCAT 802  
 233 alvalcylserProlylsasnalavalprovalillehis 246  
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 803 GTGTGTCCTATCCGAATGGACATTCCTCCACACCGCAT 843  
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seq\_documentation\_block:  
 LOCUS AV659167 789 bp mRNA linear EST 16-JAN-2002  
 DEFINITION AV659167 GLC Homo sapiens cDNA clone G1CFUB08 3', mRNA sequence.  
 ACCESSION AV659167  
 VERSION AV659167.1 GI:9880181  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 789)  
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
 Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X.,  
 Hu, G., Gu, J., Chen, Z., and Han, Z.  
 Insight into hepatocellular carcinogenesis at transcriptome level  
 by comparing gene expression profiles of hepatocellular carcinoma  
 with those of corresponding noncancerous liver  
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE  
 JOURNAL  
 MEDLINE  
 COMMENT  
 Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919(ex.45)  
 Fax: 86-21-50801922  
 Email: hanzgchgc.sh.cn  
 This clone is available at CHGC in Shanghai.

FEATURES  
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 /lab\_host="SOLR"  
 /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 268 a 140 c 162 g 210 t 9 others  
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Alignment\_scores:  
 Quality: 900.00 Length: 178  
 Ratio: 5.202 Gaps: 1

Percent Similarity: 97.191 Percent Identity: 97.191

alignment\_block:  
 US-08-917-710-2 x AV659167 ..

Align seq 1/1 to: AV659167 from: 1 to: 789

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 196 nleuserpheleullealelleuleserasnnglyasnrythrncys 213  
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 98 CTGAGTTCTCCTCATTCCTTAATTCATAATGAAATGAAATACACATG 147  
 213 alvalthrtyrprogluansgllyarg. Thrphethrleuthrargthrle 229  
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 148 TTGTTACATATCCGAAATGAGACTGACCTTTCATCCTCAGGAGACT 197  
 229 uthrvallyvalvalcylserProlylsasnalavalprovalilleh 246  
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 198 GACTGTAAAGTAGTAGGCTCTCCAAAAATGCGAGTCCCTGTGTATCC 247  
 246 lsserproasnaspheisvalvaltyrarglulysgluproglyglulneu 262  
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 248 ATTCACCTAATGATCATGTGCTATATGAAAGAACACGAGAGAGACTA 297  
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 298 CTCATTCCTCCGTACGGCTGCTATATTAGTTTCTGATGATTCCTCCAA 347  
 279 uvaltyrthrphrleasgllylyslsypasasphelethrleaspy 296  
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 348 GGTGTGTGGACCATGATGATGAAAAAACCTGATGACATCTCTTATG 397  
 296 althrileasngluserlleserhisserargthrngluaspgluthrarg 312  
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 398 TCACCATTAACGAAGTATAGTCTATAGAACGAAGATGAACAAAGA 447  
 313 thrnglileuserlilelyslsvalthrsergluaspleuysaryse 329  
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 448 ACTCAGATTNTGAGCATCAGAAAGTACCTGTGGATCTCAAGCGCAG 497  
 329 tyrtalcyshislaargseralalyglulvalalalyalaalal 346  
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 498 CTATGCTGTCTATGCTAGAAAGTCCANNAGCGCAAGTCCCAAGACGCA 547  
 346 ysvallysglnlysglyasnargcysglyln 356  
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 548 AGGTGACGACGAAGTATATAGTCGCGTCAAG 579

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 seq\_documentation\_block:  
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 DEFINITION mw96b02.r1 Soares mouse NMU Mus musculus cDNA clone IMAGE:678507 5',  
 similar to gb:X85999 M.musculus mRNA for interleukin 1 receptor  
 accessory (MUSE), mRNA sequence.

ACCESSION AA237107  
 VERSION AA237107.1 GI:1861163  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 598)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 TITLE The WashU-HMII Mouse EST Project  
 JOURNAL Unpublished (1996)

## COMMENT

Contact: Maria M/Mouse EST Project  
 Mashu-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL: contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:418211

Seq primer: -28m13 rev2 ET from Amer sham  
 High quality sequence stop: 438.

## FEATURES

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/organism="Mus musculus"  
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 was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGGCGGGAATCTTTTCTTTT 3'];  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7n3 vector. Library  
 constructed and normalized by Bento Soares and M. Fatima  
 Bernaldo."

BASE COUNT 161 a 146 c 137 g 153 t 1 others  
 ORIGIN

## alignment\_scores:

Quality: 870.50 Length: 194  
 Ratio: 4.836 Gaps: 1  
 Percent Similarity: 92.784 Percent Identity: 80.928

## alignment\_block:

US-08-917-710-2 x AA237107 ..

Align seg 1/1 to: AA237107 from: 1 to: 598

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80 uGluPProIleAsnPhesrleuProGluAsnArgIleSerLysGluLysA 97
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63 GGAGCCCATTAACCTCCGCTCCAGAGAACTGCATCAGTAAGAGAAAG 112
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97 sPValleuTTPheArGProThrLeuLeuAsnSPThrGlyAsnTYrThr 113
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113 ATGAGCTGTGTCGGCCGACCTCTCTCAATACACGGGCAATTACACC 162
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114 CysMeleuArGAsnThrThrTYrCysSerLysValAlaPheProLeuG1 130
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130 uValValGlnLysAspSerCysPheAsnSerProMetLysLeuProValH 147
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213 AGTTGTTCAGAAAGACAGCTGTTCAATTCTGCCATGAAATTCCTCCG 262
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147 IsLysLeuTYrIleGluTYrGlyIleGlnArgIleThrCysProAsnVal 163
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263 ACAAGATGATATATGAAATGCAATGATCAATGATCAATGCAATGTA 312
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164 AspGlyTYrPheProSerSerValLysProThrIleThrTYrMetG1 180
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313 GACGGTACTTCTCTCCAGTCAAAACCATGCTACTTGGTATAAAGG 362
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180 yCysTYrLysIleGlnAsnPhesAsnValIleProGluGlyMetAsnL 197
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363 TTGTACTGAATATGAGACTTTCATATATGTACTACCGGAGGCGATGACT 412
197 euSerPheleuileAlaLeuileSerAsnAsnGlyAsnTYrThrCysVal 213
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413 TGAGCTTTTCATCCCTTGTTGTTCAATACGGAATTTACATGTGTG 462
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214 ValThrTYrProGluAsnGlyArgThrPheIleLeuThrArgThrLeuTh 230
   |||
463 GTTAAATATCTCTGAAACGAGCGCTCTTCCACCTCAGCAGACTGTGAC 512
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230 rValLysValValGlySerProLysAsnAlaValProProValIleHis 247
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513 TGTAAAGGTGTGGGCTCACANAGATGCAATTCGCCACCATGATCTACT 562
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247 ePProAsnAspHisValValTYrGlyLysGlu 257
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563 CC...AATGACCGTGTGTCTATCGAAGAGAC 591

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seq\_name: gb\_est1:BB625831

## seq\_documentation\_block:

LOCUS BB625831 652 bp mRNA linear EST 31-AUG-2001  
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 musculus cDNA clone 9330131B06 5', mRNA sequence.  
 ACCESSION BB625831  
 VERSION BB625831.1 GI:15398624  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 652)  
 ARAKAWA,T., CARLINI,P., FUKUDA,S., FURUNO,M., HANAOKA,T., HARA,A.,  
 HIRAMOTO,K., HORI,F., ISHII,Y., ITO,M., KAWAI,J., KONNO,H., KOUDA,  
 M., KOYA,S., MATSUYAMA,T., MIYAZAKI,A., NOMURA,K., OHNO,M.,  
 OKAZAKI,Y., OKIDO,T., SAITO,R., SAKAI,C., SAKAI,K., SANO,H., SASAKI,  
 D., SHIBATA,K., SHINGAWA,A., SHITAKI,T., SOGABE,Y., SUZUKI,H.,  
 TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKEDA,Y., TANAKA,T., TOYA,T.,  
 MURAMATSU,M. and HAYASHIZAKI,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 CARLINI,P., SHIBATA,Y., HAYATSU,N., SUGAHARA,Y., SHIBATA,K., ITOH,  
 M., KONNO,H., OKAZAKI,Y., MURAMATSU,M. and HAYASHIZAKI,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., FUJISAKI,S., INOUE,K., TOGAWA,Y., IZAWA,M., OHARA,E.,  
 WATAHIKI,M., YONEDA,Y., ISHIKAWA,T., OZAWA,K., TANAKA,T., MATSUURA  
 S., KAWAI,J., OKAZAKI,Y., MURAMATSU,M., INOUE,Y., KIRA,A. and  
 HAYASHIZAKI,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carlini,P., Sugahara  
 Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa  
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,  
 Ishii,Y. and Hayashizaki,Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
 Func. Genomics 2 pre, L72-L86 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for

TITLE  
 JOURNAL  
 COMMENT



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**TITLE**  
**JOURNAL**  
**COMMENT**

Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel.: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.c.riken.go.jp,  
url: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
Wagii, K., Fujiwake, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E.,  
Matahiki, M., Tonedu, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
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sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*  
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Komuro, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)  
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa  
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,  
Ishii, Y. and Hayashizaki, Y.  
Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct.  
Funct. Genomics* 2 pre, 172-186 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues

**FEATURES**  
**source**

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RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGAGATCCAAAGACTCTCTTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using triehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
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ACCESSION BB653335  
VERSION BB653335.1 GI:16487192  
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SOURCE house mouse.  
ORGANISM Mus musculus  
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REFERENCE  
AUTHORS

1 (bases 1 to 676)  
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,  
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,  
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Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
Unpublished (2001)  
COMMENT  
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and  
Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system-384-format  
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Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
Y. and Hayashizaki,Y.  
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,K.I., Aizawa  
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and  
Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

#### FEATURES

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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15'  
GAGGAGAGAGAGATCCAGACCTCTTTTCTTTTCTTTTCTTTT 3', cDNA was  
prepared by using trihalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
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LOCUS AA107505 643 bp mRNA linear EST 04-NOV-1996

DEFINITION mp05d08.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA

interleukin 1 receptor accessory (MOUSE); mRNA sequence.

ACCESSION AA107505

VERSION AA107505.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The WashU-HM1 Mouse EST Project  
 Unpublished (1996)  
 Contact: Maria M/Mouse EST Project  
 WashU-HM1 Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through INL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:342983  
 Seq primer: -28M13 rev1 from Amersham  
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 Location/Qualifiers

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Wed Jun 12 09:27:08 2002

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Page 14





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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1740)
AUTHORS Cao,Z.
TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
METHODS
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VERSION	AF029213.1			
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REFERENCE	1 (bases 1 to 1740)			
AUTHORS	Huang,Y., Gao,X., Li,S. and Cao,Z.			

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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Recruitment of IRAK to the interleukin 1 receptor complex requires interleukin 1 receptor accessory protein  
Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)  
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Huang, J., Gao, X., Li, S. and Gao, Z.  
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AUTHORS Cao,Z.
TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
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 JOURNAL Submitted (31-MAR-1995) G.W. Ju, Hoffmann-La Roche Inc., 340  
 TITLE Direct Submission  
 JOURNAL 2 (bases 1 to 3355)  
 REFERENCE Kingsland Ave., Nutley, NJ 07110, USA  
 AUTHORS Greenfeder,S.A., Nunes,P., Kwee,L., Labov,M., Chizzonite,R.A. and  
 Ju,G.  
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334 laArgSerAlaLysGlyLysAlaValAlaValAlaValIysGlnLys 350
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1103 CTCGAATTCGCGAAGGAGGAGCGGACGAGCAAGCAAGCTAAGTAAACAGAAA 1152
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seq_name: gb_dr:F167333S04

seq_documentation_block:
LOCUS F167333S04 890 bp DNA linear PRI 24-MAY-2000
DEFINITION Homo sapiens Interleukin 1 receptor accessory protein (IL1RAP)
ACCESSION AF167336
VERSION AF167336.1 GI:8050492
KEYWORDS
SEGMENT
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 890)
AUTHORS Jensen,L.E., Muzio,M., Mantovani,A. and Whitehead,A.S.
TITLE IL-1 signaling cascade in liver cells and the involvement of a
soluble form of the IL-1 receptor accessory protein
JOURNAL J. Immunol. 164 (10), 5277-5286 (2000)
MEDLINE 20261666
PUBMED 10799889
REFERENCE
2 (bases 1 to 890)
AUTHORS Jensen,L.E.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-1999) Department of Pharmacology, University of
Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk,
Philadelphia, PA 19104, USA
FEATURES
source location/Qualifiers
1..890

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Ratio: 5.552 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.958
alignment_block:
US-08-917-710-2 x F167333S04
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|||||
38 eGluaspGluProAlaArgIleLysCysProLeuPheGluHisPheLeu 55
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586 TGAAGATGAGCAGACCTCGCATCAAGTCCACCTTTGAACACTTCTTGA 635
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55 yspheasnTyrSerThrAlaHisSerAlaGlyLeuThrIleuThrTyr 71
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636 AATTCAACTACAGCACGCCCATTCACCTGCTCTCTGATCTGATCTGAT 685
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72 TrpThrLysGlnaspArgaspLeuGluProIleasnPheArgLeuThr 88
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686 TGGACTGAGCAGACCGGACCTTGAAGAGCAATTAATTCGCTCC 735
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736 CGAAGAACCGCATTAAGTAAGAGAAAGATGCTGTGTTCCGCGCACAC 785
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786 TCCTCAATGACCTGGCACTATCACTGATGTTAAG 823
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seq_name: gb_htg:AC108747

seq_documentation_block:
LOCUS AC108747 160441 bp DNA linear HTG 31-JAN-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-268E23, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
ACCESSION AC108747
VERSION AC108747.1 GI:18449881
KEYWORDS
SOURCE HTG: HTGS_PHASE1, HTGS_DRAFT.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 160441)
AUTHORS Muzny,D.M., Adams,C., Adio-Ondola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayala,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Dayila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,D.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J.,

```

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,  
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
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Sutton, A., Svalek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
Tatton, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
Umani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R.,  
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,  
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

Unpublished  
Direct Submission  
2 (bases 1 to 160441)  
Worley, K.C.  
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: HDWO  
Center clone name: RP11-268E23  
----- Summary Statistics  
Sequencing vector: Plasmid; M77789  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329First call to  
findPhrapList  
Consensus quality: 159407 bases at least Q40  
Consensus quality: 160755 bases at least Q30  
Consensus quality: 161605 bases at least Q20  
Estimated insert size: 159008; sum-of-coverage estimation  
Quality coverage: 0x in Q20 bases; sum-of-coverage estimation  
Quality coverage: 5x in Q20 bases; sum-of-coverage estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 50778: contig of 50778 bp in length  
\* 50779 50878: gap of unknown length  
\* 50879 72649: contig of 21771 bp in length  
\* 72650 72749: gap of unknown length  
\* 72750 86636: contig of 13887 bp in length  
\* 86637 86736: gap of unknown length  
\* 86737 104474: contig of 17738 bp in length  
\* 104475 104574: gap of unknown length  
\* 104575 114831: contig of 10257 bp in length  
\* 114832 114931: gap of unknown length  
\* 114932 119623: contig of 4692 bp in length

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BASE COUNT 51635 a 29440 c 29448 g 46607 t 1311 others  
ORIGIN

alignment\_scores:  
Quality: 533.00 Length: 96  
Ratio: 5.552 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.958

alignment\_block:  
US-08-917-710-2 x AC108747/rev ..

Align seg 1/1 to reverse of: AC108747 from: 1 to: 160441

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38 egluaspgiuproalaargilelscysproleuphegnhispheul 55  
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8046 TGAAGTAGGACGACGCTGCATCAAGTCCCACTTTGACACTTCTGA 7997  
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55 yspheasntyserserthralahiseraaglyleuthleuthleupyr 71  
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7996 AATTCAACTACAGACAGCCATTCAGCTGCGCTTACCTGATCGGAT 7947  
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72 TTPHTLYGLASPARGASPLEUGLUGIUPROILEASNPHEARGLEUPR 88  
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7946 TGGACTAGGACGAGACCGGACCTTGAGAGGCCAATTACTCGGCTCC 7897  
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88 ogluasatrgileserlysglulysaspyalleutrpheargprothrL 105  
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7896 CGGAACCCGATAGTAGAGAGAAAGATGTGCTGTCGCGCCACTGC 7847  
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seq\_documentation\_block:  
LOCUS AC008249 184203 bp DNA linear PRI 28-OCT-1999  
DEFINITION Homo sapiens 3q27 BAC RPc11-211P13 (Koswell Park Cancer Institute  
Human BAC Library) complete sequence.  
ACCESSION AC008249  
VERSION AC008249.14 GI:6137875  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 184203)

Muzny, D.M., Adams, C., Bailey, M., Barabara, J., Blankenburg, K.,  
Bodeta, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunc, C.,  
Burgett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,  
David, R., Delgado, O., Deshaize, D., Ding, Y., Domah-Rashid, N.,  
Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,  
Fortum-Tansley, J., Frantz, P., Ganesh, R., Garcia, D.K., Gorrell, J.H.,  
Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J.,  
Hodgson, A., Hogue, M., Holloway, C., Hosak, H., Jackson, L.E.,  
Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondrjewski, N., Kong, Y.,  
Kovar, C., Leal, B., Li, Z., Lichte, O., Liu, J., Liu, W., Logan, O.,  
Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mel, G.,  
Moore, S., Moorish, T., Morgan, M., Morris, S., Nash, S., Nelson, A.,  
Nguyen, R., Nguyen, N., Nguyen, S., Oswald, G., Parish, B., Paxton, S.,  
Payton, B., Perez, L., Pu, L.L., Quiles, M., Reiter, D., Rives, M.,  
Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M.,  
Sparkes, A., Stamps, A., Sugand, R., Tabor, P., Taylor, T., Vasquez, L.,  
Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstein, G.,  
Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrenford, G.,  
Yu, W., Zhou, X., Zou, S.L., Nelson, D. and Gibbs, R.

TITLE  
JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 184203)

## AUTHORS

Worley, K.C.

TITLE  
JOURNAL

Direct Submission

Submitted (30-JUL-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 184203)

## AUTHORS

Worley, K.C.

TITLE  
JOURNAL

Direct Submission

Submitted (28-OCT-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Oct 28, 1999 this sequence version replaced gi:6091634.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
[gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the  
entire insert of this clone. Overlapping regions of clones are only  
sequenced and submitted once, so the sequence for the remainder of  
the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the  
Features listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches  
of a local database that includes entries from dbSTS, GDB, and  
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST  
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
EST and cDNA sequences. Genes demonstrate at least two exons  
flanked by consensus splice sites that maintained sequence  
continuity across the splice junctions. Sequences that are not  
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
standard of double strand coverage with a minimum of 2 clones and 2  
reads with no ambiguities or 2 chemistries with a minimum of 2  
clones and 3 reads with no ambiguities. If the sequence quality for  
a region does not meet this standard, it will be indicated in the  
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
standards - estimated error rate less than 1 per 10,000 bases.  
Reports of lowest quality individual bases and measures of base  
quality are listed below. Description of the metrics can be found  
at URL: [http://gc.bcm.tmc.edu:8088/quality\\_info/genbank\\_annotation.html](http://gc.bcm.tmc.edu:8088/quality_info/genbank_annotation.html).

QUALSTAT-REPORT-----

Summary Statistics	
Contig Length:	184203
Phrap values in estimate:	183529
Average error rate (BCM-Phrap estimate):	1.29501e-05
Fraction of Phrap values less than 40 :	0.0125648
Number of consensus changing edits:	4
Number of N's in consensus :	0

  

Consensus Changing edits	
Position	Original+Context
6949	aaggagactg(n)acaactctt
148395	tctatattg(t)tttatctct
171291	gagagaagaa(n)caactgacta
171310	taagcatg(a)agcaattagg

  

Distribution of Quality < 40 Bases	
#	Phrap Value Range
1000	5 10 15 20 25 30 35 40
900	*
800	*
700	*
600	*
500	*
400	*
300	*
200	*
100	*
0	*

  

Version: 1.01 gxf.	
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	/chromosome="3q27"
	/clone="RPCL11-211P13"
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	/rpt_family="L1MD1"
repeat_region	complement(1665..1737)
	/rpt_family="L1MMA4"
repeat_region	2744..3103
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repeat_region	complement(3102..3340)
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repeat_region	complement(3819..4105)
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repeat_region	5595..5615
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Align seg 1/1 to: AF212016 from: 1 to: 2061

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859 ..... TTATTGAGAGACTGGCAGGTCCACATTAGA...GAAGG 893
309 pGluThrArg.....ThrGlnI 315
894 TGAATAAAGGCTTTCMAAGACATCTTGAGCAAAAAGACTGAATTGG 943
315 IeLuSerIleLysIlyValThrSerGluasPLeuIlyArgSerTyrVal 331
944 CATCTCATCTTTGACTCAGTTGTGGAAGCTGAACCTG...GCCAATTATACC 990
332 CysHisAlaArgSerAlaLysGlyIuValAlaLysAlaIaLysValIly 348
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348 scLnIyrs 350
1041 TAAAAAG 1047

seq_name: gb_pr:HS290436

seq_documentation_block:
LOCUS          HSA290436          2080 bp      mRNA      linear      PRI 13-NOV-2001
DEFINITION     Homo sapiens mRNA for ILIRAPL-2 related protein.
ACCESSION      AJ290436
VERSION        AJ290436.1  GI:7688204
KEYWORDS       ILIRAPL-2 gene; ILIRAPL-2 related protein.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (sites)
AUTHORS        Ferrante,M.I., Ghiani,M., Bulfone,A. and Franco,B.
TITLE          ILIRAPL2 maps to Xq22 and is specifically expressed in the central
               nervous system
JOURNAL        Gene 275 (2), 217-221 (2001)
MEDLINE        21472256
REFERENCE      2 (bases 1 to 2080)
AUTHORS        Ferrante,M.
TITLE          Direct Submission
JOURNAL        Submitted (02-MAY-2000) Ferrante M., Telethon Institute of
               Genetics and Medicine, via Olgettina, 58, 20132 Milano, ITALY
FEATURES
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922..1067,1068..1211,1212..1382,1383..2080)
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[illegible][illegible]

259 yglJLglnLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspS 276  
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793 TAAGCCTGTGAACATCCCGTCGAAACCATTTCTTCGGATTTCAGTGGAGACT 842

276 erargasngluValIrpirpintIeasprylylsysfionshpasprie 222

293 ThrIleAsnValThrIleAsnGluSerIleSerHisSerArgThrGluAs 309

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878 .....TTTATGAGAACTGGCAGGTACATTAGA...GAAGG 912
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309 pglTharg.....Thrgni 315
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913 TGAATTAAGCGTCCTCTCAAAAGCATCTTGAGAAAAAGACTGTGATTGG 967
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315 leleuserIeLysValThrSerGlnAspLeuLysArgSerGlyVal 333
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963 CACTCATCTTTGAGCTCAGTGTGGAAGCTGACCCTG...GCCATTATACC 1007

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220 AAGAGAAATTCGTGGATGGCTGCATTCAGTGGCGATGGAT...CTCA 266  
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66 uThrLeuIleTyrTrpThrLysGlnAspArgAspLeuGluuProI 83  
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116 uArgAsnThrThrTyrCysSerLysValAlaPheProLeuGluValAlG 133  
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505 AAGAACTCAACAATATGCTAGAAAGGTGCAATGCTTCATCGTTGGAC 554  
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133 LntLysAspSer...CysPheAsnSerProMetLysLeuProValHis 147  
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593 .....TATTATGAAATATGTGAGTCACTCACTAAAGAAAGAGATCTCTG 636  
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160 sProAsnValAspGlyTyrPheProSerSerValLysProThrIleMetH 177  
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637 TCCAGACATGATGATCACTTAAAAAGTCCGATCGAGGCCGATGTGTGTG 686  
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177 rPtyMetGlyCysTyrLysIleGlnAspHeaAsnValIleProGlu 193  
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687 GGTATAGGAATGCAAGCCAAAAATGNGGAGAGCATTAATATACGAAG 736  
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194 GluMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTy 210  
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737 GGAATGCTCTTGTGATCCACAGAAGTTCACAGAAGAGATGGAGAAACTA 786  
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210 rThrCysValValThrTyrProGluAsnGlyArgThrPheHisLeuThA 227  
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787 CACATGTGAACCTAATAT...GAAGAAACT...GTAAAGC 824  
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825 GAACAACCTGAAATGAAAGTTACAGCTTACTACAGACCAAGCTCCCAAG 874  
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243 ProValIleHisSerProAsnAspHisValValTyrGluGlnGlyProG 259  
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875 CCAATGTGTCOCACATGGAGATACGCCAAGTGTATATGATGTCCAGGTGG 924  
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259 yGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspS 276  
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925 TAAAGCTTGAAATATCCCTGCAAAAGCATTTTCGATTCAGTGGAGAGT 974  
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276 eArgAsnGluValIlePTrpThrIleAspGlyLysProAspSple 292  
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975 CTGGCCCATGATCTATGG...ATGAAAGGAGAAAG..... 1009  
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DEFINITION Homo sapiens mRNA for IL-1 receptor accessory protein-like 2
(ILI1RAPI-2 gene).
ACCESSION AJ272208
VERSION AJ272208.1 GI:7530096
KEYWORDS IL1RAPI-2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2985)
TITLE Grabowski,M., Lorenz,B., Hubel,R. and Strom,T.M.
JOURNAL A gene (ILI1RAPI-2) with 61% identity to IL1RAPI maps to Xq22.2
AUTHORS Unpublished
2 (bases 1 to 2985)
Strom,T.M.
TITLE Direct Submission
AUTHORS Submitted (14-FEB-2000) Strom T.M., Medizinische Genetik,
JOURNAL Getheistr. 29, Muenchen 80336, GERMANY
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